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OM protein - protein search, using sw model

Run on: January 6, 2002, 09:47:04 ; Search time 22.43 Seconds (without alignments)

82.561 Million cell updates/sec

Title:	US-09-441-061-2
Perfect score:	125
Sequence:	1 GMAALPRLIAFTSEHSFSLKGA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 220984
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Minimum DB seq length: 0
Maximum DB seq length: 25

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Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 50 summaries

Database : A_Geneseq_1101:4

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1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT *
2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT *
3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT *
4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT *
5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT *
6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT *
7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT *
8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT *
9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT *
10: /SID52/gcgdata/geneseq/geneseq/AA1989.DAT *
11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT *
12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT *
13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT *
14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT *
15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT *
16: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT *
17: /SID52/gcgdata/geneseq/geneseq/AA1996.DAT *
18: /SID52/gcgdata/geneseq/geneseq/AA1997.DAT *
19: /SID52/gcgdata/geneseq/geneseq/AA1998.DAT *
20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT *
21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT *
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	125	100.0	25	16	AA888667	Human glutamic ac
2	125	100.0	25	18	AAW18848	KD glutamic ac
3	82	65.6	20	16	AA822279	Glutamic acid dec
4	82	65.6	20	21	AA959532	GAD65 fragment, p
5	67	53.6	20	16	AA872278	Glutamic acid dec
6	67	53.6	20	21	AA959578	GAD65 fragment, p
7	64	51.2	20	21	AA857065	Glutamate decarbo
8	39	31.2	24	21	AA807785	Glutamic acid dec
9	37.5	30.0	15	22	AA861512	HCW type 16 anti
10	37	29.6	15	19	AA865435	Helper T-cell cla
11	37	29.6	15	21	AA873095	Hepatitis C virus

12	37	29.6	15	22	AAJ03084	Hepatitis C virus
13	37	29.6	15	22	AAJ03390	Hepatitis C virus
14	37	29.6	15	22	AAJ04014	Hepatitis C virus
15	37	29.6	15	22	AAJ04073	Hepatitis C virus
16	37	29.6	15	17	AAJ01981	Antigenic peptide
17	37	29.6	22	21	AAJ73093	Hepatitis C virus
18	37	29.6	22	21	AAJ04072	Hepatitis C virus
19	37	29.6	24	14	AAJ84063	HCV NS peptide DP3
20	35	28.0	19	20	AAJ1898	Rheumatoid arthritis
21	34	27.2	11	22	AAJ02448	Hepatitis C virus
22	34	27.2	11	22	AAJ02837	Hepatitis C virus
23	34	27.2	21	19	AAJ85304	Helper T-cell class
24	34	27.2	21	21	AAJ73094	Hepatitis C virus
25	34	27.2	21	21	AAJ82059	HCV antigen, NS4.1
26	34	27.2	21	22	AAJ00020	Hepatitis C virus
27	34	27.2	21	22	AAJ04047	Hepatitis C virus
28	34	27.2	21	22	AAJ04074	Hepatitis C virus
29	34	27.2	21	22	AAJ04114	Hepatitis C virus
30	34	27.2	22	14	AAJ41115	HCV peptide NS4e.
31	33.5	26.8	9	22	AAJ86153	HCV type 16 antigen
32	33.5	26.8	15	22	AAJ86151	HCV type 16 antigen
33	33	26.4	17	7	AAJ60774	Sequence 2 encoded
34	33	26.4	24	13	AAJ82662	GAD peptide. Synt
35	33	26.4	24	21	AAJ824165	Rat liver 6-pyruvo
36	33	26.4	12	21	AAJ07784	Glutamic acid deca
37	31	24.8	14	20	AAJ05598	HIV-1 group O stra
38	31	24.8	15	19	AAJ56030	ICH-3 p20 region 1
39	31	24.8	17	9	AAJ81134	HLV-PX-related pe
40	31	24.8	18	15	AAJ9369	HLA-DR beta-chain
41	31	24.8	22	21	AAJ54605	AV37 antigen prote
42	31	24.8	23	19	AAJ50098	Human chorionic go
43	31	24.8	23	19	AAJ50063	Human chorionic go
44	31	24.8	23	20	AAJ55619	HIV-1 group O stra
45	31	24.8	25	20	AAJ36603	Fragment of human
46	31	24.8	25	22	AAJ4293	peptide #777 encod
47	31	24.8	25	22	AAJ26703	peptide #740 encod
48	31	24.8	25	22	AAJ04084	Human cDNA partial
49	31	24.8	25	22	AAJ02022	peptide #704 encod
50	30.5	24.4	9	22	AAJ86154	HCV type 16 antigen

ALIGNMENTS

RESULT	1
AAR88667	
ID	AAR88667 standard; peptide; 25 AA

AC AAR88667

DT 05-MAR-1996 (first entry)

Human glutamic acid decarboxylase residues 266-290.

	diabetes; T-cell subpopulation; detection; antigen production
KW	diagnosis; autoimmune disease.
KW	

OS Homo sapiens.

PN DE4418091-A1

PD 27-JUL-1995.

PF 24-MAY-1994; 94DE-4418091.

PR 04-FEB-1994; 94DE-4403522.

PA (BOEF) BOEHRINGER MANNHEIM

PI Albert W, Dornmaier K, Endl J, Jung G, Meinel E,

RESULT 4
AAV59552
ID AAV59552 standard; peptide; 20 AA.
XX
AC AAV59552;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #19.
XX
KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW Insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN US5998366-A.
XX
PD 07-DEC-1999.
XX
PF 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX
DR WPI; 2000-095930/08.
XX
PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders, such as insulin dependent diabetes mellitus and Stiff man
PT disease -
XX
XX Claim 1; Column 42; 61pp; English.
XX
PS
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and Stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
CC
XX
SQ Sequence 20 AA;

Query Match 65.6%; Score 82; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSPSLKGA 25
DB 1 AFTSEHSPSLKGA 16

RESULT 5
AAV59578
ID AAV59578 standard; peptide; 20 AA.
XX
AC AAV59578;
XX
DT 13-NOV-1995 (first entry)
XX
DE Glutamic acid decarboxylase (GAD65) fragment.
XX
KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
KW

KW Insulin-dependent diabetes mellitus; stiff man disease.
XX
OS Homo sapiens.
XX
PN WO9507992-A.
XX
PD 23-MAR-1995.
XX
PF 24-AUG-1994; 94WO-US09478.
XX
PR 17-SEP-1993; 93US-0123859.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
XX
DR WPI; 1995-131360/17.
XX
PT New polypeptide fragments of glutamic acid decarboxylase - for
PT diagnosis and treatment of autoimmune disease, esp. insulin
PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hydridoma(s) etc.
XX
PS Example 11; Page 76; 100pp; English.
XX
CC AA086481 and AA086482 encode AAR71733 and AAR79105, rat and human
CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in AAR72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.
XX
SQ Sequence 20 AA;

Query Match 53.6%; Score 67; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTE 14
DB 7 gmaalprliafste 20

RESULT 6
AAV59578
ID AAV59578 standard; peptide; 20 AA.
XX
AC AAV59578;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #18.
XX
KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW Insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN US5998366-A.
XX
PD 07-DEC-1999.
XX
PF 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;

XX WPI; 2000-095930/08.
 DR Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and Stiff man
 PT disease -
 XX
 PS Example 11; Column 42; 61pp; English.
 XX
 CC This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.
 XX
 SQ Sequence 20 AA;

Query Match 53.6%; Score 67; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMAALPRLIAFTSE 14
 DB 7 gmaalprliaftse 20
 |||||:|||||

RESULT 7
 AAY57065
 ID AAY57065 standard; peptide; 20 AA.
 XX
 AC AAY57065;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Glutamate decarboxylase peptide GAD p18.
 XX
 KW Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.
 XX
 OS Homo sapiens.
 XX
 PN WO9956763-A1..
 XX
 PD 11-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US10250.
 XX
 PR 07-MAY-1998; 98US-0084636.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Kaufman DL, Tian J, Olcott A;
 XX
 DR WPI; 2000-052905/04.
 XX
 PT Administration of neglected target tissue antigens to modulate immune
 PT responses -
 XX
 PS Disclosure; Page 23; 79pp; English.
 XX

XX Amino acid sequences AAY57063-Y57091 are examples of neglected target
 CC tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)
 CC not involved in autoimmunity. These peptides and proteins are used in
 CC the method of the invention which involves administering an NNTA as an

CC antigen based immunotherapeutic agent, to a host afflicted with an
 CC autoimmune response associated with an autoimmune disease. The
 CC immunotherapeutic agent is used to treat autoimmune diseases such as
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
 CC inflammatory immune responses. The NNTA induces regulatory tolerance by
 CC elicitation of regulatory T cells among T cells recognizing the NNTA but
 CC not participating in the immune response. The NNTA are capable of
 CC recognition by substantial populations of uncommitted T cells which can
 CC be primed, or biased, towards regulatory responses to provide effective
 CC treatment. The NNTA are effective in regulating undesirable immune
 CC responses even when target determinants used as agents promoting
 CC tolerance agents have failed to induce an effective regulatory T cell
 CC response. NNTAs as agents promoting tolerance are anticipated to be safer
 CC than use of target determinants.

XX Sequence 20 AA;

Query Match 51.2%; Score 64; DB 21; Length 20;
 Best Local Similarity 92.9%; Pred. No. 0.00025;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMAALPRLIAFTSE 14
 DB 7 gmaalprliaftse 20
 |||||:|||||

RESULT 8
 AAB07785
 ID AAB07785 standard; peptide; 24 AA.
 XX
 AC AAB07785;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Glutamic acid decarboxylase-65 (GAD-65) analogue peptide.
 XX
 KW Glutamic acid decarboxylase-65; GAD-65; autoimmune disease;
 KW insulin-dependent diabetes mellitus; IDDM; stiff man syndrome;
 KW cellular autoimmune response; T-cell receptor; autoimmune antigen.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 15
 FT /label= Thr, Glu

XX EP1026238-A2.

XX 09-AUG-2000.

XX 17-JUN-1992; 2000EP-0102229.

XX 18-JUN-1991; 91US-0716909.

XX 17-JUN-1992; 92EP-0110308.

XX (REGC) UNIV CALIFORNIA.

XX Tobin AJ, Erlander MG, Kaufman DL, Clare-salzler MJ;

XX WPI; 2000-500251/45.

XX Diagnosing and treating autoimmune diseases such as insulin-dependent
 PT diabetes mellitus and detecting antibodies to glutamin acid
 PT decarboxylase (GAD)65 in a sample, using GAD65 polypeptide -

XX Claim 15; Page -; 32pp; English.

XX The specification describes a method which uses a glutamic acid
 CC decarboxylase-65 (GAD-65) polypeptide or analogue for diagnosing and
 CC treating autoimmune diseases such as insulin-dependent diabetes
 CC mellitus (IDDM). The polypeptide is useful for diagnosing IDDM and

CC for the preparation of medicament for treating IDDM or stiff man
CC syndrome; detecting antibodies (preferably autoantibodies to GAD-65).
CC It is also useful for classifying patients with autoimmune diseases
CC such as IDDM, screening drugs that alters GAD function, generation of
CC an antibody preferably monoclonal or polyclonal autoantibodies, blocking
CC cellular autoimmune responses, blocking recognition by a specific T-cell
CC receptor or a major histocompatibility complex (MHC) receptor presenting
CC an autoantigen on the surface of an antigen presenting cell,
CC stimulating a T-suppressor cell population, and competing for recognition
CC of self-antigens at a level of antigen presentation. The present
CC sequence represents a GAD-65 analogue of the invention.
CC note: the present sequence does not appear in the specification; it was
CC created using information provided.

XX Sequence 24 AA;

Query Match 31.2%; Score 39; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMAALPRL 8
| | | | |
DB 17 gmaalprl.24

RESULT 9

ID AAB46152 standard; peptide; 15 AA.

AC AAB46152;

DT 04-APR-2001 (first entry)

DE HCMV type 16 antigenic peptide SEQ ID NO 20.

XX Antigenic; vaccine; Interferon-gamma; tumor necrosis factor-alpha;

KW CD8+ T cell; HCMV infection; immune response.

XX Human cytomegalovirus.

XX WO200075180-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-DE01854.

PR 04-JUN-1999; 99DE-1027039.

PR 07-SEP-1999; 99DE-1043702.

PA (KERN/) KERN F.

PI Kern F, Volk H, Relinke P, Faulhaber N, Sural I, Khatazmas E;

PI WPI; 2001-061700/07.

PT New peptides that stimulate cytokine production in T cells, useful for

PT vaccination against human cytomegalovirus infection and for detecting

PT immune responses to the virus

PS Claim 1; Page 26; 28pp; German.

CC This invention describes novel peptides (I), their encoding DNA (II) or
CC their derivatives, that stimulate production of interferon-gamma and
CC tumor necrosis factor-alpha in CD8+ T cells, particularly those from
CC humans of suitable HLA type who have been immunized with human
CC cytomegalovirus (HCMV). (I) and their derivatives are used for
CC therapeutic or prophylactic vaccination against HCMV infection and as
CC diagnostic reagents for detecting or quantifying the cellular immune
CC response to HCMV (from ability to induce production of the specific
CC cytokines in CD8+ cells), particularly in immune-deficient subjects. Also
CC DNAs (II) that encode (I), and vectors and plasmids containing (II), are
CC useful as pharmaceuticals.

XX Sequence 15 AA;

Query Match 30.0%; Score 37.5; DB 22; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 9 IAFSESHFSL 20
| | | | |
DB 2 vafts-hehfgl 12

RESULT 10

ID AAW85435 standard; peptide; 15 AA.

AC AAW85435;

DT 16-FEB-1999 (first entry)

DE Helper T-cell class II peptide derived from NS4 protein.

XX Helper T-cell peptide; human leucocyte antigen; HLA; DR4*4; DR1;

KW DR7; cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;

KW acquired immune deficiency syndrome; malaria; cancer;

KW allograft rejection; allergy; Lyme disease; hepatitis;

KW post-streptococcal endocarditis; glomerulonephritis;

XX food hypersensitivity.

XX Synthetic.

OS Hepatitis C virus.

XX WO9832456-A1.

PD 30-JUL-1998.

PF 23-JAN-1998; 98WO-US01373.

PR 07-FEB-1997; 97US-0037432.

PR 23-JAN-1997; 97US-0036713.

PA (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S;

PI WPI; 1998-427679/36.

PT Composition containing peptide that induces cytotoxic T lymphocyte

PT response, and helper peptide - can bind to human leucocyte antigen

PT alleles, used to treat or prevent cancers, parasitic infections and

PT autoimmune disease

PS Disclosure; Page 42; 51pp; English.

CC AAW85284-451 represent helper T-cell class II peptides, which can bind
CC to the human leucocyte antigens (HLA) DR4*4, DR1 and DR7. The peptides
CC are used in the course of the invention. The specification describes
CC peptides that induce a cytotoxic T lymphocyte (CTL) response, and
CC T-helper peptides, that are used together to generate a CTL response for
CC the treatment or prevention of viral, fungal, bacterial or parasitic
CC infections (e.g. hepatitis, acquired immune deficiency syndrome or
CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate
CC cancer or condyloma acuminatum). Helper T-cell peptides may be used
CC alone to induce a helper T cell response, e.g. in cases of autoimmune
CC disease, allograft rejection, allergy, Lyme disease, hepatitis,
CC post-streptococcal endocarditis, glomerulonephritis and food
CC hypersensitivity.

Query Match 29.6%; Score 37; DB 19; Length 15;

10

AC AA03390;
XX
PI 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #3381.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US19774.
XX
PR 19-JUL-1999; 99US-0357737.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccine against hepatitis C virus
XX
PS Disclosure; Page 177; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 RLIAFTSEHSFHS 19
DB 3 RLIAFTSEHSFHS 15

RESULT 14
AAJ04014
ID AAJ04014 standard; Peptide; 15 AA.
XX
AC AAJ04014;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #4005.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US19774.
XX
PR 19-JUL-1999; 99US-0357737.
XX
PA (EPIM-) EPIMUNE INC.
XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccine against hepatitis C virus
XX
PS Example 5; Page 198; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 RLIAFTSEHSFHS 19
DB 3 RLIAFTSEHSFHS 15

RESULT 15
AAJ04073
ID AAJ04073 standard; Peptide; 15 AA.
XX
AC AAJ04073;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #4064.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US19774.
XX
PR 19-JUL-1999; 99US-0357737.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccine against hepatitis C virus
XX
PS Example 5; Page 201; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSFHS 19
||||| : | |
Db 3 rliafasrghvs 15

RESULT 16

AAW01981
ID AAW01981 standard; peptide; 20 AA.

XX AC AAW01981;

DT 26-SEP-1996 (first entry)

DE Antigenic peptide comprising HCV NS4 protein residues 1916-1935.

XX Antigenic peptide; C-terminal region; hepatitis C virus; HCV;
KW non-A non-B; non-structural protein 4; NS4; differential diagnosis;
KW acute; chronic; infection; binding assay.

XX Hepatitis C virus.

DE WO9604300-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-US09599.

XX 29-JUL-1994; 94US-0282758.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA (USSH) US SEC DEPT HEALTH.

PI Fields HA, Khudyakov YE;

XX WPI; 1996-129330/13.

XX Antigenic peptide(s) binding anti-hepatitis C virus antibodies
PT useful for differential diagnosis of HCV in subjects

PS Claim 3; Page 27; 50pp; English.

XX The present peptide is an antigenic peptide (AP), derived from the
CC C-terminal region of the hepatitis C virus (HCV) non-structural
CC protein 4 (NS4). The AP was prep. using Fmoc chemistry, and can be
CC used in a claimed method for the differential diagnosis of HCV.
CC One, two or three of the peptides AAW01980-82 are separately
CC contacted with an antibody (Ab) contg. sample, and the binding
CC between the peptide(s) and the Ab determined. The Ab contg. sample
CC is then contacted with the peptide AAW01983, and the binding between
CC the peptide and the Ab determined. The strength of the binding
CC between the peptide(s) and the Ab in the two assays is compared,
CC where stronger binding in the 1st assay is indicative of acute HCV
CC infection, and equivalent binding is indicative of chronic HCV
CC infection.

XX Sequence 20 AA;

Query Match 29.6%; Score 37; DB 17; Length 20;

Best Local Similarity 61.5%; Pred. No. 12;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSFHS 19
||||| : | |
Db 3 rliafasrghvs 15

RESULT 17

AAV73093
ID AAV73093 standard; Peptide; 22 AA.

XX AAV73093;

XX

DT 28-FEB-2000 (first entry)

XX Hepatitis C virus (HCV)-derived MHC class II (HTL) epitope, #251.

DE Chimeric; pan DR epitope; expression vector;

XX promoter; major histocompatibility complex; MHC; targeting; peptide;
KW epitope; antigen; presentation; class I; cytosolic pathway;

XX endoplasmic reticulum; class II; extracellular antigen;

XX endocytic pathway; helper T lymphocyte; HTL; universal epitope;

XX cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;

XX vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;

XX hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;

XX autoimmune disease; activation; antiviral; antimalarial;

XX immunoprotective.

XX Synthetic.

OS Hepatitis C virus.

XX WO9958658-A2.

PN 18-NOV-1999.

XX 13-MAY-1999; 99WO-US10646.

XX 13-MAY-1998; 98US-0078904.

XX 15-MAY-1998; 98US-0085751.

XX (EPIM-) EPIMUNE INC.

XX Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;

PI Chesnut RW;

XX WPI; 2000-039103/03.

XX Expression vectors encoding major histocompatibility targeting

PT sequence, used as, e.g. tumor vaccines -

XX Claim 11; Page 67; 130pp; English.

XX Sequences AAV73087-Y73102 represent hepatitis C virus (HCV)-derived MHC
CC class II (HTL) epitopes which are claimed for use in the present
CC invention. The invention relates to a novel expression vector comprising
CC a promoter operably linked to a fusion gene encoding a major
CC histocompatibility complex (MHC) targeting sequence, and two or more
CC heterologous peptide epitopes. The MHC targeting sequence may be a
CC class I targeting sequence, which directs an MHC class I epitope to
CC a cytosolic pathway or to the endoplasmic reticulum, or an MHC class
CC II targeting sequence, which directs extracellular antigens to
CC enter the endocytic pathway to be processed into antigen peptides
CC for presentation on MHC class II molecules. The heterologous
CC epitopes may comprise either helper T lymphocyte (HTL) epitopes,
CC or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
CC epitope such as a pan DR epitope (PADRE). The vectors are useful
CC for stimulating an immune response in vivo, as well as for use in
CC assaying the human immunogenicity of a human T cell peptide epitope in
CC vivo in a non-human mammal. They provide a nucleic acid vaccine for
CC enhancing immunity against infectious pathogens, such as viruses (e.g.,
CC HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g.,
CC Plasmodium falciparum, the cause of malaria) and also tumour cells and
CC autoimmune diseases. Universal MHC class II epitopes are advantageously
CC combined with other MHC class I and class II epitopes to increase the
CC number of cells that are activated in response to a given antigen and
CC provide a broader population coverage of MHC-reactive alleles.

XX Sequence 22 AA;

Query Match

Best Local Similarity 29.6%; Score 37; DB 21; Length 22;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSFHS 19

Db 10 rliatfasrghvs 22

RESULT 18

AAJ04072 standard; Peptide; 22 AA.

AAJ04072;

02-JUL-2001 (first entry)

Hepatitis C virus epitope #4063.

Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;

antiviral.

Hepatitis C virus.

WO200121189-A1.

29-MAR-2001.

19-JUL-2000; 2000WO-US19774.

19-JUL-1999; 99US-0357737.

(EPIM-) EPIMUNE INC.

Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

Baker DM, Celis E, Kubo RT, Grey HM;

WPI; 2001-308046/32.

A new composition useful as a vaccine against hepatitis C virus

Example 5; Page 201; 214pp; English.

The present invention describes a composition comprising a prepared

hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.

These are derived from HCV HLA-binding motifs. They are useful in

vaccines for the prevention and treatment of HCV infection in humans. The

present sequence is an epitope used in the disclosure of the invention.

Sequence 22 AA;

Query Match 29.6%; Score 37; DB 22; Length 22;

Best Local Similarity 61.5%; Pred. No. 14;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

7 RLIAFTSEHSFHS 19

10 rliatfasrghvs 22

RESULT 19

AAAR34043 standard; peptide; 24 AA.

AAAR34043;

22-JUL-1993 (first entry)

HCV NS peptide DP3.

Hepatitis C virus; non structural region; antigen; diagnosis; vaccine.

Synthetic.

WO9306488-A.

01-APR-1993.

16-SEP-1992; 92WO-US07865.

16-SEP-1991; 91US-0762135.

12-FEB-1992; 92US-0835717.

(GENE-) GENELABS TECHNOLOGIES INC.

Burk KH, Dreesman GR, Pauletti D;

WPI; 1993-117737/14.

Detection of hepatitis C virus antigens - using HCV reactive

antibody bound to solid support and competitive HCV

antigen-reporter complex

Claim 27; Page 122; 190pp; English.

The synthetic peptide corresponds to residues 1917-1940 of the NS4

domain of HCV. The peptide may be used for the sensitive and

specific detection of HCV infection. Antibodies raised against the

peptide can be used for passive immuno-prophylaxis and the HCV

antigens can be used in vaccines to prevent HCV infection.

See also AAR34041-65.

Sequence 24 AA;

7 RLIAFTSEHSFHS 19

2 rliatfasrghvs 14

RESULT 20

AAV41898

AAV41898 standard; Peptide; 19 AA.

AAV41898;

09-DEC-1999 (first entry)

Rheumatoid arthritis diagnostic protein isoform peptide #49.

Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;

rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;

rheumatoid arthritis diagnostic protein isoform; screening;

expression reference protein isoform; prognosis.

Homo sapiens.

WO9947925-A2.

23-SEP-1999.

15-MAR-1999; 99WO-GB00763.

13-MAR-1998; 98GB-0005477.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Parekh RB, Patel TP, Townsend RR;

WPI; 1999-571871/48.

Diagnosis of human rheumatoid arthritis by two-dimensional

electrophoresis -

Disclosure; Page 18; 157pp; English.

CC A method has been developed for the diagnosis of human rheumatoid
 CC arthritis (RA) using two-dimensional electrophoresis to generate a
 CC two-dimensional array of features. The method can be used for screening,
 CC diagnosis and prognosis of RA in a subject or for monitoring the effect
 CC of an anti-RA drug or therapy administered to a subject. The method
 CC comprises: (a) analysing a sample of serum or plasma and optionally
 CC synovial fluid by two-dimensional electrophoresis, to generate a two-
 CC dimensional array of features; (b) identifying at least one chosen
 CC feature whose relative abundance correlates with the presence or absence
 CC of RA; and (c) comparing the abundance of each chosen feature in the
 CC sample with the abundance of that chosen feature in serum or plasma from
 CC one or more persons without RA, where the relative abundance of the
 CC chosen feature or features in the sample indicates the presence or
 CC absence of RA in the subject. The method can also be used in clinical
 CC studies for testing drugs for therapy of RA, for purification of RA-
 CC diagnostic protein isoforms (RPIs), and for production of antibodies to
 CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
 CC compounds that promote or inhibit their activity, which are then used as
 CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
 CC protocols. RAY41844 to AAY42100 represent RPI peptides, AAY42101 to
 CC AAY42103 represent expression reference protein isoform peptides and
 CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
 CC used in the exemplification of the present invention.

XX Sequence 19 AA;

Query Match 28.0%; Score 35; DB 20; Length 19;
 Best Local Similarity 43.8%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 LIATSEHSFSLKKG 23
 ||: ||||: | : |
 Db 1 llsvötehsnlylqng 16

RESULT 21

AAJ02448
 ID AAJ02448 standard; Peptide; 11 AA.

XX AC AAJ02448;

XX 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #2439.

XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.

OS Hepatitis C virus.

XX WO200121189-A1.

XX 29-MAR-2001.

PF 19-JUL-2000; 2000WO-US19774.

XX 19-JUL-1999; 99US-0357737.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cells E, Kubo RT, Grey HM;

XX WPI; 2001-308046/32.

XX A new composition useful as a vaccine against hepatitis C virus

PT Disclosure; Page 160; 214pp; English.

XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in

CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.

XX Sequence 11 AA;

Query Match 27.2%; Score 34; DB 22; Length 11;
 Best Local Similarity 63.6%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSH 17
 ||||| | : |
 Db 1 rliafasrghn 11

RESULT 22

AAJ02837
 ID AAJ02837 standard; Peptide; 11 AA.

XX AC AAJ02837;

XX 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #2828.

XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.

OS Hepatitis C virus.

XX WO200121189-A1.

XX 29-MAR-2001.

PF 19-JUL-2000; 2000WO-US19774.

XX 19-JUL-1999; 99US-0357737.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cells E, Kubo RT, Grey HM;

XX WPI; 2001-308046/32.

XX A new composition useful as a vaccine against hepatitis C virus

PS Disclosure; Page 169; 214pp; English.

XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.

XX Sequence 11 AA;

Query Match 27.2%; Score 34; DB 22; Length 11;
 Best Local Similarity 63.6%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSH 17
 ||||| | : |
 Db 1 rliafasrghn 11

RESULT 23

AAW85304
 ID AAW85304 standard; peptide; 21 AA.

XX AC AAW85304;

XX AAW85304;

ID AAB82059 standard; peptide; 21 AA.
 XX
 AC AAB82059;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE HCV antigen, NS4 1909-1929.
 XX
 KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
 XX viral infection.
 OS Hepatitis c virus.
 XX
 PN WO200124822-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 02-OCT-2000; 2000WO-EP09657.
 XX
 PR 01-OCT-1999; 99AT-0001680.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Fleitmann J, Mattner F, Buschle M, Melling J;
 XX
 DR WPI; 2001-290577/30.
 XX
 PT New pharmaceutical composition comprising an antigen, an
 PT immunostimulating substance and a polycationic polymer, useful in
 PT manufacturing vaccines
 XX
 PS Claim 12; Page 16; 20pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC (a) an antigen; (b) an immunostimulating substance consisting of
 CC neuroactive compounds, hormones, compounds having growth hormone activity
 CC or their mixtures; and (c) a polycationic polymer. The present sequence
 CC is an antigenic peptide derived from Hepatitis c virus, which was used in
 CC the present invention. The composition is useful in manufacturing
 CC vaccines.
 XX
 SQ Sequence 21 AA;

Query Match 27.2%; Score 34; DB 22; Length 21;
 Best Local Similarity 63.6%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 7 RLIAFTSEHSH 17
 ||||| :
 Db 10 RLIAFASRQNH 20

Search completed: January 6, 2002, 09:51:45
 Job time: 281 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 6, 2002, 09:48:44 ; Search time 17.04 Seconds
(without alignments)
33.015 Million cell updates/sec

Title: US-09-441-061-2
Sequence: 125
1 GMAALPRLAFTSEHSHSLKGA 25

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 123821

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: Issued Patents, AA:
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	65.6	20	2	US-08-484-530-32
2	82	65.6	20	2	US-08-827-618A-32
3	82	65.6	20	3	US-08-483-952A-32
4	67	53.6	20	2	US-08-484-530-31
5	67	53.6	20	2	US-08-827-618A-31
6	67	53.6	20	3	US-08-483-952A-31
7	40	32.0	10	3	US-08-159-339A-933
8	39	31.2	8	6	5475086-14
9	39	31.2	24	1	US-08-485-718-2
10	39	31.2	24	2	US-08-484-530-2
11	39	31.2	24	2	US-08-827-618A-2
12	39	31.2	24	3	US-08-483-952A-2
13	37	29.6	20	1	US-08-282-758B-2
14	37	29.6	24	5	PCT-US92-07865-3
15	35	28.0	9	3	US-08-159-339A-915
16	35	28.0	10	3	US-08-159-339A-1031
17	34	27.2	9	3	US-08-159-339A-978
18	34	27.2	22	2	US-08-146-028-58
19	34	27.2	22	4	US-08-723-425A-58
20	34	27.2	22	4	US-09-112-206-58
21	33	26.4	23	1	US-08-485-718-1
22	33	26.4	23	2	US-08-484-530-1
23	33	26.4	23	2	US-08-827-618A-1
24	33	26.4	23	3	US-08-483-952A-1
25	33	26.4	24	6	5475086-8
26	33	25.6	14	1	US-07-690-983D-24
27	32	25.6	24	1	US-07-690-983D-43

28	31	24.8	11	1	US-08-411-727-4	Sequence 4, App1
29	31	24.8	13	5	PCT-US92-09070-7	Sequence 7, App1
30	31	24.8	15	4	US-08-908-436-7	Sequence 7, App1
31	31	24.8	18	2	US-08-480-190-79	Sequence 79, App1
32	31	24.8	18	2	US-08-488-379-79	Sequence 79, App1
33	31	24.8	18	5	PCT-US93-07545-79	Sequence 1008, Ap
34	30	24.0	9	3	US-08-159-339A-1008	Sequence 1008, Ap
35	30	24.0	9	3	US-08-159-339A-1009	Sequence 1009, Ap
36	29	23.2	10	2	US-08-107-676-5	Sequence 962, App
37	29	23.2	10	3	US-08-159-339A-962	Sequence 69, App1
38	29	23.2	11	3	US-08-467-580-69	Sequence 69, App1
39	29	23.2	11	5	PCT-US95-08516-69	Sequence 16, App1
40	29	23.2	14	1	US-07-909-122-16	Sequence 5, App1
41	29	23.2	20	1	US-07-678-974D-5	Sequence 7, App1
42	29	23.2	20	1	US-08-199-508-7	Sequence 117, App
43	29	23.2	20	2	US-08-934-915-117	Sequence 145, App
44	29	23.2	20	2	US-08-934-915-145	Sequence 10, App1
45	29	23.2	20	2	US-08-945-168-10	Sequence 5, App1
46	29	23.2	22	3	US-09-093-227-5	Patent No. 5283320
47	29	23.2	23	6	5283320-7	Sequence 22, App1
48	28.5	22.8	21	4	US-09-143-124-22	Sequence 30, App1
49	28	22.4	11	3	US-08-467-580-30	Sequence 30, App1
50	28	22.4	11	5	PCT-US95-08516-30	Sequence 30, App1

ALIGNMENTS

RESULT 1
US-08-484-530-32
; Sequence 32, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:
; APPLICANT: Toblin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albrighton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,530
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacatlin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-530-32
; Query Match 65.6%; Score 82; DB 2; Length 20;
; Best Local Similarity 100.0%; Pred. No. 7.4e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSHFLKKGAA 25
Db 1 AFTSEHSHFLKKGAA 16

RESULT 2

US-08-827-618A-32
; Sequence 32, Application US/08827618A
; Patent No. 5998366
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,618A
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,725
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/716,909
; FILING DATE: 18-JUN-1991

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/586,536
; FILING DATE: 21-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-618A-32

Query Match 65.6%; Score 82; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0;

QY 10 AFTSEHSHFLKKGAA 25
Db 1 AFTSEHSHFLKKGAA 16

RESULT 3

US-08-483-952A-32
; Sequence 32, Application US/08483952A
; Patent No. 6011139
; GENERAL INFORMATION:

APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,952A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,859
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/716,909
; FILING DATE: 18-JUN-1991

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/586,536
; FILING DATE: 21-SEP-1990
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-952A-32

Query Match 65.6%; Score 82; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSHFLKKGAA 25
Db 1 AFTSEHSHFLKKGAA 16

RESULT 4

US-08-484-530-31
; Sequence 31, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:

APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-31

Query Match 53.6%; Score 67; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
|||||
DB 7 GMAALPRLIAFTSE 20

RESULT 5
US-08-827-618A-31
Sequence 31, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-31

Query Match 53.6%; Score 67; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
|||||
DB 7 GMAALPRLIAFTSE 20

RESULT 6
US-08-483-952A-31
Sequence 31, Application US/08483952A
Patent No. 601139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-483-952A-31

Query Match 53.6%; Score 67; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLAFTSE 14
Db 7 GMAALPRLAFTSE 20
|||||

RESULT 7
US-08-159-339A-933
; Sequence 933, Application US/08159339A
; Patent No. 6037135

;; GENERAL INFORMATION:
;; APPLICANT: Kubo, Ralph T.
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Celis, Esteban
;; TITLE OF INVENTION: HLA Binding peptides and Their
;; NUMBER OF SEQUENCES: 1254
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111-3834

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/159,339A
;; FILING DATE: 29-NOV-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/926,666
;; FILING DATE: 07-AUG-1992
;; APPLICATION NUMBER: US 08/027,746
;; FILING DATE: 05-MAR-1993
;; APPLICATION NUMBER: US 08/103,396
;; FILING DATE: 06-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Ellen Lauver
;; REGISTRATION NUMBER: 32,762
;; REFERENCE/DOCKET NUMBER: 018623-00503003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 933:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-159-339A-933

Query Match 32.0%; Score 40; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 TSESHFSLK 21
Db 1 TSEQSHYSIK 10
|||||

RESULT 8
5475086-14

;; APPLICANT: TOBIN, ALLAN J.;ERLANDER, MARK G.;KAUFMAN,
;; DANIEL L.;CLARE-SALZLER, MICHAEL J.
;; TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
;; PEPTIDES

;; NUMBER OF SEQUENCES: 14
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/135,849
;; FILING DATE: 13-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 716,909
;; FILING DATE: 18-JUN-1991
;; APPLICATION NUMBER: 586,536
;; FILING DATE: 21-SEP-1990

;; SEQ ID NO:14:
;; LENGTH: 8
5475086-14

Query Match 31.2%; Score 39; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8
Db 1 GMAALPRL 8
|||||

RESULT 9

US-08-485-718-2
; Sequence 2, Application US/08485718
; Patent No. 5705626

;; GENERAL INFORMATION:
;; APPLICANT: Tobin, Allan J.
;; APPLICANT: Erlander, Mark G.
;; APPLICANT: Kaufman, Daniel L.
;; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;; STREET: Four Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94111-4187

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/485,718
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland, Bertram I
;; REGISTRATION NUMBER: 20015
;; REFERENCE/DOCKET NUMBER: A60780-6/BIR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-781-1989
;; TELEFAX: 415-398-3249

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids
;; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-718-2

Query Match 31.2%; Score 39; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 10
US-08-484-530-2
Sequence 2, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-530-2

Query Match 31.2%; Score 39; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 11
US-08-827-618A-2
Sequence 2, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,309
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-827-618A-2

Query Match 31.2%; Score 39; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 12
US-08-483-952A-2
Sequence 2, Application US/08483952A
Patent No. 6011139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-952A-2

Query Match 31.2%; Score 39; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 13
US-08-282-758B-2
Sequence 2, Application US/08282758B
Patent No. 5670310
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Khudyakov, Yuri B.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Differential Diagnosis of Chronic and Acute Hepatitis C
TITLE OF INVENTION: Virus Infection
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,758B
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Green, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-282-758B-2

Query Match 29.6%; Score 37; DB 1; Length 20;
Best Local Similarity 61.5%; Pred. No. 4.6;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 RLIAFTSEHSFS 19
Db 3 RLIAFASGRNHS 15

RESULT 14
PCT-US92-07865-3
Sequence 3, Application PC/TUS9207865
GENERAL INFORMATION:
APPLICANT: Dreesman, Gordon R.
APPLICANT: Burk, Kenneth H.
APPLICANT: Pauletti, Daniel
TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
NUMBER OF SEQUENCES: 25
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07865
FILING DATE: 19920916
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 16-SEP-1991
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 1600-0086.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal

ORIGINAL SOURCE:
ORGANISM: Hepatitis C Virus
INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
INDIVIDUAL ISOLATE: HCV polyprotein
PCR-US92-07865-3

Query Match 29.6%; Score 37; DB 5; Length 24;
Best Local Similarity 61.5%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIAFTEHSFHS 19
|||||:|
DB 2 RLIAFASRGNHVS 14

RESULT 15
US-08-159-339A-915
Sequence 915, Application US/08159339A
Patent No. 6037135;

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159, 339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926, 666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027, 746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103, 396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX:

INFORMATION FOR SEQ ID NO: 915:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-159-339A-915

Query Match 28.0%; Score 35; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 TSEHSFSL 20
|||||:
DB 1 TSEQSHYSI 9

RESULT 16
US-08-159-339A-1031
Sequence 1031, Application US/08159339A
Patent No. 6037135;

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.

APPLICANT: Sette, Alessandro

APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding peptides and Their

TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159, 339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926, 666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027, 746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103, 396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX:

INFORMATION FOR SEQ ID NO: 1031:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-159-339A-1031

Query Match 28.0%; Score 35; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 MAAPRLIAF 11
|||||:
DB 1 MAAPKLVLF 10

RESULT 17
US-08-159-339A-978
Sequence 978, Application US/08159339A
Patent No. 6037135;

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.

APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES OR BIOTINYLATED
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; FEATURE:

; SOFTWARE: PatentIn Release #1.0, Version #1.23 (EPO)

NAME/KEY: Modified-site
LOCATION: 1
FEATURE: Modified-site
NAME/KEY: Modified-site
LOCATION: 22
US-08-723-425A-58

Query Match 27.2%; Score 34; DB 4; Length 22;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLIAFTSESH 17
| | | | | : |
Db 11 RLIAFASRGNH 21

RESULT 20
US-09-112-206-58
Sequence 58, Application US/09112206
Patent No. 6210903
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112,206

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,028
FILING DATE:

INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV

FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 22
US-09-112-206-58

Query Match 27.2%; Score 34; DB 4; Length 22;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLIAFTSESH 17
| | | | | : |
Db 11 RLIAFASRGNH 21

RESULT 21
US-08-485-718-1
Sequence 1, Application US/08485718
Patent No. 5705626
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.

APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Honbach, Test, Aldritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US

ZIP: 94111-4187
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,718
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertam I

REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-6/BIR

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-718-1

Query Match 26.4%; Score 33; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8
| | | | | : |
Db 16 GMAAVPKL 23

RESULT 22
US-08-484-530-1
Sequence 1, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:

APPLICANT: Tobin, Allan J
APPLICANT: Kaufman, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Honbach, Test, Aldritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US

ZIP: 94111-4187
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RET/MTK
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-1

Query Match 26.4%; Score 33; DB 2; Length 23;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8
Db 16 GMAAVPKL 23

RESULT 23
US-08-827-618A-1
Sequence 1, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Kaufman, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-APR-1997
APPLICATION NUMBER: US/08/827,618A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RET/MTK
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-827-618A-1

Query Match 26.4%; Score 33; DB 2; Length 23;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8
Db 16 GMAAVPKL 23

RESULT 24
US-08-483-952A-1
Sequence 1, Application US/08483952A
Patent No. 6011139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Kaufman, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RET/MTK
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-1

Query Match 26.4%; Score 33; DB 3; Length 23;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8

Db 16 GMAAVPKL 23

RESULT 25

5475086-8

Patent No. 5475086

APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN, DANIEL L.; CLARE-SALZLER, MICHAEL J.

TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE PEPTIDES

NUMBER OF SEQUENCES: 14

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/135,849

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 716,909

FILING DATE: 18-JUN-1991

APPLICATION NUMBER: 586,536

FILING DATE: 21-SEP-1990

SEQ ID NO: 8

LENGTH: 24

5475086-8

Query Match 26.4%; Score 33; DB 6; Length 24;

Best Local Similarity 75.0%; Pred. No. 28;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8

Db 17 GMAAVPKL 24

Search completed: January 6, 2002, 09:52:30
job time: 226 sec

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OM protein - protein search, using sw model

Run on: January 6, 2002, 09:49:29 ; Search time 19.62 Seconds
(without alignments)
97.062 Million cell updates/sec

Title: US-09-441-061-2
Perfect score: 125
Sequence: 1 GMAALPRLIATSEHSRSLKKGAA 25

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174553 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database : PIR 68:.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	25.6	25	2	H64710
2	29	23.2	20	2	S03954
3	27	21.6	14	2	PS0249
4	26	20.8	10	2	PC2171
5	26	20.8	22	2	B39138
6	26	20.8	24	2	I73619
7	25	20.0	8	2	XGHEU
8	25	20.0	22	2	A28563
9	24.5	19.6	20	2	S07232
10	24	19.2	20	2	A53875
11	24	19.2	22	2	S40638
12	24	19.2	22	2	F84018
13	24	19.2	25	2	U00361
14	24	18.4	14	2	A60770
15	23	18.4	15	2	PS0455
16	23	18.4	15	2	PT0094
17	23	18.4	18	2	S66227
18	23	18.4	22	2	A17267
19	23	18.4	22	2	H66433
20	23	18.4	23	2	PH0858
21	23	18.4	24	2	A36912
22	23	18.4	24	4	S09363
23	22	17.6	10	2	S74176
24	22	17.6	12	2	S01122
25	22	17.6	12	2	PH1635
26	22	17.6	13	2	B61620
27	22	17.6	15	2	PA0087
28	22	17.6	16	2	A85827
29	22	17.6	18	2	S48862

30	22	17.6	19	2	S43652
31	22	17.6	20	2	B41299
32	22	17.6	20	2	A85645
33	22	17.6	22	2	S59071
34	22	17.6	22	2	I37144
35	22	17.6	23	2	S51188
36	22	17.6	25	2	A10759
37	22	17.6	25	2	S36378
38	21.5	17.2	21	2	PH1641
39	21.5	17.2	23	4	A35039
40	21	16.8	6	4	A38929
41	21	16.8	13	2	A38929
42	21	16.8	13	2	H56046
43	21	16.8	16	1	LEFCH
44	21	16.8	16	2	C39509
45	21	16.8	16	2	C61414
46	21	16.8	17	2	B61414
47	21	16.8	18	2	B48408
48	21	16.8	19	2	S59717
49	21	16.8	20	2	S78760
50	21	16.8	22	2	PT0070

ALIGNMENTS

RESULT 1
H64710
hypothetical protein HP1528 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: H64710
R:Tomb, J.F.; White, O.; Keriavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, J.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khakh, H.G.; Glodek, A.; McK.
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey
Nature 388, 539-547, 1997
A:Authors: Wallin, E., Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: H64710
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-25 <TOM>
A:Cross-references: GB:AE000651; GB:AE000511; NID:92314708; PIDN:AMD08577.1; PID:9231

Query Match 25.6%; Score 32; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 8 LIAPFSEHSRSLKKG 23
DB 2 LIAPFSEHSRSLKKG 17

RESULT 2
S03954
acidic fibroblast growth factor - pig (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03954
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethke, N.; Sharma, H.S.; Sc.
Eur. J. Biochem. 181, 67-73, 1989
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine
A:Reference number: S03953; MUID:89231704
A:Accession: S03954
A:Molecule type: protein
A:Residues: 1-20 <OUT>
C:Keywords: growth factor

Query Match 23.2%; Score 29; DB 2; Length 20;

Best Local Similarity 35.7%; Pred. No. 3e+02; Mismatches 3; Indels 6; Gaps 0;

QY 5 LPRLIAFTSEHSF 18
| | : : | |
Db 3 LPPKLYSSNGGHF 16

RESULT 3

PS0249
porin - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C:Accession: PS0249

R:Tsugita, A.

submitted to JIPID, April 1993

A:Reference number: PS0206

A:Accession: PS0249

A:Molecule type: protein

A:Residues: 1-14 <TSU>

A:Experimental source: callus

Query Match 21.6%; Score 27; DB 2; Length 14;

Best Local Similarity 30.8%; Pred. No. 4.3e+02;

Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 9 IAFTEHSFSLK 21

| | : : | |

Db 2 VTFTDHTANGIK 14

RESULT 4

PC2171

triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragment)

C:Species: Rhizopus niveus

C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C:Accession: PC2171

R:Kohno, M.; Kugamiya, W.; Hashimoto, Y.; Morita, Y.

Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994

A:Title: Purification, characterization, and crystallization of two types of lipase from

A:Reference number: PC2171; MUID:94319059

A:Accession: PC2171

A:Molecule type: protein

A:Residues: 1-10 <KOR>

C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds.

C:Keywords: carboxylic ester hydrolase

Query Match 20.8%; Score 26; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 4.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AALPLIA 10

| | | | |

Db 3 AALPLIS 10

RESULT 5

B39138

dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Pelobacter carbinolicus (fragment)

C:Species: Pelobacter carbinolicus

C>Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 05-May-2000

C:Accession: B39138

R:Oppermann, F.B.; Schmidt, B.; Steinbuechel, A.

J. Bacteriol. 173, 757-767, 1991

A:Title: Purification and characterization of acetoin:2,6-dichlorophenolindophenol oxid

s acetoin dehydrogenase enzyme system.

A:Reference number: A39138; MUID:91100366

A:Accession: B39138

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-22 <OPP>

C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C:Keywords: acyltransferase; coenzyme A

Query Match 20.8%; Score 26; DB 2; Length 22;

Best Local Similarity 29.4%; Pred. No. 1e+03;

Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSFLKKG 23

| : | | | : : | |

Db 4 RLIAFTPKKGLTMEEG 20

RESULT 6

I73619

endothelial growth factor receptors flt [imported] - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000

C:Accession: I73619

R:Boockock, C.A.; Charnock-Jones, D.S.; Sharkey, A.M.; McLaren, J.; Barker, P.J.; Wr

J. Natl. Cancer Inst. 87, 506-516, 1995

A:Title: Expression of vascular endothelial growth factor and its receptors flt and

A:Reference number: 156493; MUID:95222657

A:Accession: I73619

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-24 <RES>

A:Cross-references: GB:S77814; NID:g998566; PIDN:AAB34002.1; PID:g998567

C:Genetics:

A:Gene: flt

Query Match 20.8%; Score 26; DB 2; Length 24;

Best Local Similarity 44.4%; Pred. No. 1.1e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 AFTSEHSF 18

: | : | |

Db 14 SFSSNYVHF 22

RESULT 7

XGHUEU

urine glycopeptide - human

C:Species: Homo sapiens (man)

C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: A03188

R:Lothe, C.J.; Weiss, J.B.

Biochem. J. 123, 25P, 1971

A:Title: Identification in urine of a low-molecular-weight polar glycopeptide conta

A:Reference number: A03188; MUID:72062338

A:Accession: A03188

A:Molecule type: protein

A:Residues: 1-8 <LOT>

C:Comment: The identity of the glycoprotein from which this peptide is derived is u

re has also been found (see PIR:XGHUE).

C:Superfamily: unassigned animal peptides

C:Keywords: glycoprotein

F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 20.0%; Score 25; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 EHSF 17

| | | | |

Db 2 EHSF 5

RESULT 8

A28563

hemoglobin chain III - earthworm (Lumbricus terrestris) (fragment)

C:Species: Lumbricus terrestris (common earthworm)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 04-Mar-2000
C:Accession: A28563

R:Gotoh, T.; Shishikura, F.; Snow, J.W.; Ertel, K.I.; Vinogradov, S.N.; Walz, D.A.
Biochem. J. 241, 441-445, 1987
A:Title: Two globin strains in the giant annelid extracellular haemoglobins.
A:Reference number: A90337; MUID:87241210

A:Accession: A28563
A:Molecule type: protein
A:Residues: 1-22 <GOT>
C:Superfamily: globin; globin homology
C:Keywords: oxygen carrier

Query Match 20.0%; Score 25; DB 2; Length 22;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 13 SEHSFSLK 22
||| : : :
Db 8 SEEDHYVOK 17

RESULT 9
S07232
ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - garden pea (frag
N:Alternate names: rubisco subunit-binding protein alpha chain
C:Species: Pisum sativum (garden pea)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C:Accession: S07232
R:Musgrove, J.E.; Johnson, R.A.; Ellis, R.J.
Eur. J. Biochem. 163, 529-534, 1987
A:Title: Dissociation of the ribulosebiphosphate-carboxylase large-subunit binding prot
A:Reference number: S07232; MUID:87161853
A:Accession: S07232
A:Molecule type: protein
A:Residues: 1-20 <MUS>
C:Comment: This protein binds the newly synthesized large subunit and the newly imported
C:Superfamily: chaperonin GROEL
C:Keywords: chloroplast; heterododecamer; molecular chaperone

Query Match 19.6%; Score 24.5; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

OY 9 IAFSEHSFSLK 23
||| : : :
Db 5 IAF-DQHSRAMQNG 18

RESULT 10
A53875
creative kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997
C:Accession: A53875
R:White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.
J. Protein Chem. 11, 489-494, 1992
A:Title: The principal islet of the Coho salmon (*Oncorhynchus kisutch*) contains the BB is
A:Reference number: A53875; MUID:93080727
A:Accession: A53875
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-20 <WHI>
A:Experimental source: Brockmann body, principal islet
A:Note: sequence extracted from NCBI backbone (NCBIP:120599)
C:Superfamily: creatine kinase; creatine kinase repeat homology
C:Keywords: phosphotransferase

Query Match 19.2%; Score 24; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 11 FTSEHSFSL 20
| : | : | :
Db 2 FGNTHNFKL 11

RESULT 11
S40638
ARF-43 protein - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S40638
R:Hurst, H.C.; Tolly, N.F.; Jones, N.C.
Nucleic Acids Res. 19, 4601-4609, 1991
A:Title: Identification and functional characterization of the cellular activating t
A:Reference number: S40638; MUID:91367654
A:Accession: S40638
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-22 <HUR>

Query Match 19.2%; Score 24; DB 2; Length 22;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 ALPRLAFTS 13
||| : : :
Db 13 SLPTQVMTS 22

RESULT 12
F84018
hypothetical protein BH2950 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: F84018
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A83650; MUID:20263314
A:Accession: F84018
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <STO>
A:Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06669.1; GSPDB:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2950

Query Match 19.2%; Score 24; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 18 FSLKKG 23
||| : : :
Db 8 FSLKKG 13

RESULT 13
J00361
vasoactive intestinal peptide - Atlantic cod (fragment)
C:Species: Gadus morhua (Atlantic cod)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Nov-1997
C:Accession: J00361
R:Thwaites, D.T.; Young, J.; Thorndyke, M.C.; Dimaline, R.
Regul. Pept. 21, 436, 1988
A:Title: Isolation and characterisation of two teleost VIP's.
A:Reference number: J00361
A:Accession: J00361

RESULT 19

H86433

protein T17H7.9 [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: H86433

R:Proteologs, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: H86433

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <STD>

A:Cross-references: GB:AE005172; NID:g4926824; PIDN:AAD32934.1; GSPDB:GN00141

C:Genetics:

A:Gene: T17H7.9

A:Map position: 1

Query Match 18.4%; Score 23; DB 2; Length 22;
 Best Local Similarity 62.5%; Pred. No. 3.1e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 SEHSFSL 20

Db 13 SERNFSL 20

RESULT 20

PH0858

Maud protein - Paracoccus denitrificans (fragment)

C:Species: Paracoccus denitrificans

C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999

C:Accession: PH0858

R:Christodov, A.Y.; Boyd, J.; Matthews, F.S.; Lidstrom, M.E.
 Biochem. Biophys. Res. Commun. 184, 1181-1189, 1992

A:Title: The genetic organization of the mau gene cluster of the facultative autotroph F

A:Reference number: PH0856; MUID:92272706
 A:Accession: PH0858

A:Molecule type: DNA

A:Residues: 1-23 <CH>

A:Cross-references: GB:M90098; NID:g150580; PIDN:AAA25577.1; PID:g150581
 C:Genetics:

A:Gene: mauD

Query Match 18.4%; Score 23; DB 2; Length 23;
 Best Local Similarity 36.0%; Pred. No. 3.2e+03;

Matches 9; Conservative 3; Mismatches 5; Indels 8; Gaps 1;

QY 1 GMAALPRLIAFTSEHSIKKGA 25

Db 7 GPASLQQTMA-----SRKQNA 23

RESULT 21

A36912

hypothetical protein 1 batg-region [Imported] - Eubacterium sp. (fragment)

C:Species: Eubacterium sp.

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C:Accession: A36912

R:Franklund, C.V.; Baron, S.F.; Hylemon, P.B.
 J. Bacteriol. 175, 3002-3012, 1993

A:Title: Characterization of the batg gene encoding a bile acid-inducible NADH:flavin ox
 A:Reference number: A36912; MUID:93259945

A:Accession: A36912

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-24 <RFA>

A:Experimental source: VPI 12708

A:Note: sequence extracted from NCBI backbone (NCBIN:131883, NCBI:P:131906)

Query Match 18.4%; Score 23; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LPRLIAFTSE 14

Db 4 LPVLIIFLQ 13

RESULT 22

S09363

hypothetical MTCO1/MTCYB mutant fusion protein - human mitochondrion (fragment)

C:Species: mitochondrion Homo sapiens (man)

C:Date: 21-Nov-1993 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000

C:Accession: S09363

R:Poulton, J.; Deadman, M.E.; Gardiner, R.M.
 Nucleic Acids Res. 17, 10223-10229, 1989

A:Title: Tandem direct duplications of mitochondrial DNA in mitochondrial myopathy:
 A:Reference number: S09363; MUID:90098864

A:Accession: S09363

A:Molecule type: DNA

A:Residues: 1-24 <POU>

C:Comment: This is the hypothetical translation of a sequence believed to result fro

C:Genetics:

A:Gene: MTCO1/MTCYB

A:genome: mitochondrion

A:genetic code: SGC1

C:Keywords: fusion protein; mitochondrion
 F:1-4/Region: cytochrome-c oxidase chain I
 F:5-24/Region: cytochrome b (+2 frame shifted)

Query Match 18.4%; Score 23; DB 4; Length 24;
 Best Local Similarity 66.7%; Pred. No. 3.4e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 17 HFSIKK 22

Db 7 HFSRKK 12

RESULT 23

S74176

gluconokinase (EC 2.7.1.12), thermoresistant - Escherichia coli (fragment)

C:Species: Escherichia coli

C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999

C:Accession: S74176

R:izu, H.; Adachi, O.; Yamada, M.
 FEBS Lett. 394, 14-16, 1996

A:Title: Purification and characterization of the Escherichia coli thermoresistant g
 A:Reference number: S74176; MUID:97074194

A:Accession: S74176

A:Molecule type: protein

A:Residues: 1-10 <ID>

A:Experimental source: strain K-12
 C:Genetics:

A:Gene: gntK

C:Keywords: dimer; phosphotransferase

Query Match 17.6%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2e+03;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 TSESH 17

```

Db      2  TTNHDS 7
      1: 1 1
RESULT 24
S01122
Photosystem II 3.7K protein - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: S01122
R;Schroeder, W.P.; Henrysson, T.; Akerlund, H.E.
FEBS Lett. 235, 289-292, 1988
A;Title: Characterization of low molecular mass proteins of photosystem II by N-terminal
A;Reference number: S01120
A;Accession: S01122
A;Molecule type: protein
A;Residues: 1-12 <SCH>
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match      17.6%; Score 22; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  5  LPRLIAFTS 13
Db      2  LPEAYAFLS 10
      1 1 1 1 1 1
RESULT 25
PH1635
Ig H chain V-D-J region (clone B-less 218) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1635
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609
A;Accession: PH1635
A;Molecule type: DNA
A;Residues: 1-12 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match      17.6%; Score 22; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  3  AALPRLIAF 11
Db      2  AGLPGLLYC 10
      1 1 1 1 1
Search completed: January 6, 2002, 09:53:18
Job time: 229 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2002, 09:52:34 ; Search time 12.98 Seconds

(without alignments)
70.618 Million cell updates/sec

Title: US-09-441-061-2
Perfect score: 125
Sequence: 1 GMAALPRLIAFTSEHSFLKKGAA 25

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.5	22.8	21	1	MISG_MISAN
2	26	20.8	25	1	CR11_LITSP
3	26	20.8	25	1	CR12_LITCE
4	26	20.8	25	1	CR13_LITCE
5	26	20.8	25	1	CR14_LITGI
6	25	20.0	8	1	GLOR_HUMAN
7	25	20.0	24	1	FRF4_LITIN
8	24	19.2	25	1	CR15_LITCE
9	24	19.2	25	1	VIP_GADMO
10	23	18.4	12	1	PVR2_PPRAM
11	23	18.4	22	1	CO4_CAVPO
12	22.5	18.0	23	1	CH60_THIFE
13	22	17.6	13	1	LMT4_LOCM1
14	22	17.6	18	1	CYCH_MOUSE
15	21	16.8	8	1	FAR7_ASCSU
16	21	16.8	16	1	LPH1_ECOLI
17	21	16.8	22	1	SETB_SALTU
18	21	16.8	24	1	GAB6_RANRU
19	20	16.0	8	1	ALP1_CYDPO
20	20	16.0	10	1	GLEK_HUMAN
21	20	16.0	10	1	GONI_PETMA
22	20	16.0	15	1	ASPL_LACSN
23	20	16.0	15	1	MCA2_RHOOP
24	20	16.0	20	1	DFTS_RAT
25	20	16.0	22	1	LPTB_BACST
26	20	16.0	22	1	CYSP_TRIVA
27	20	16.0	24	1	LPER_SRRFR
28	20	16.0	25	1	SCRK_LACLA
29	19.5	15.6	25	1	G3P2_JACOR
30	19	15.2	10	1	GONI_ALIMI
31	19	15.2	16	1	CXAL_CONAL
32	19	15.2	18	1	AL13_CARMA
33	19	15.2	19	1	ATPB_CANFA

34	19	15.2	19	1	COXR_THUOB
35	19	15.2	20	1	CD4_SHEEP
36	19	15.2	20	1	RNKD_PIG
37	19	15.2	22	1	MIP_RANFE
38	19	15.2	24	1	ATPE_MICLU
39	19	15.2	24	1	VGU_BPALJ
40	19	15.2	25	1	COXO_ONCMY
41	18	14.4	9	1	PEK1_PPRAM
42	18	14.4	10	1	UPA4_HUMAN
43	18	14.4	12	1	UKA2_HUMAN
44	18	14.4	13	1	CXA2_CONCE
45	18	14.4	13	1	ODPA_CANFA
46	18	14.4	14	1	MAST_VESXA
47	18	14.4	14	1	MY14_EISFO
48	18	14.4	14	1	PH1_PRUSE
49	18	14.4	14	1	PK6_PPRAM
50	18	14.4	15	1	LPH1_ECOLI

ALIGNMENTS

RESULT 1
ID MISG_MISAN STANDARD; PRT; 21 AA.
AC P81474;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MISGURIN.
OS Misgurnus anguillicaudatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cobitidae; Misgurnus.
OX NCBI_TaxID=75329;
RN [1]
RP SEQUENCE.
RX MEDLINE=97415401; PubMed=9271200;
RA Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;
RT "A novel antimicrobial peptide from the loach, Misgurnus
RT anguillicaudatus.";
RL FEBS Lett. 411:173-178(1997).
CC -1- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL
CC -1- GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI.
CC -1- MASS SPECTROMETRY: MW=2502; METHOD=MALDI.
KW Antibiotic; Fungicide.
SQ SEQUENCE 21 AA; 2502 MW; 4A6E9D0AB391BCF1 CRC64;

Query Match 22.8%; Score 28.5; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 14 EHSFSLKKGAA 25
DB 6 ELSKFS-KKGAA 16

RESULT 2
ID CR11_LITSP STANDARD; PRT; 25 AA.
AC P56226;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 1.1.
OS Litoria splendida, Litoria gilleni, and Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OX Litoria.
OX NCBI_TaxID=30345, 39405, 30344;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1 AND 1.1.2.

RC SPECIES-L.splendida; TISSUE-Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. Structures of the caerins and
 ceridin 1 from Litoria splendida";
 RL J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).
 RN [2]
 RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1; 1.1.2 AND 1.1.4.
 RC SPECIES-L.caerulea; TISSUE-Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea";
 RL J. Chem. Res. 138:910-936(1993).
 RN [3]
 RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1; 1.1.3; 1.1.5 TO 1.1.8.
 RC SPECIES-L.gilleni; TISSUE-Parotoid gland;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins and
 ceridins from Litoria gilleni";
 RL J. Chem. Res. 139:937-961(1993).
 RN [4]
 RP FUNCTION, AND STRUCTURE BY NMR.
 RC SPECIES-L.splendida;
 RX MEDLINE-97409981; PubMed-9266696;
 RA Wong H., Bowie J.H., Carver J.A.;
 RT "The solution structure and activity of caerin 1.1, an antimicrobial
 peptide from the Australian green tree frog, Litoria splendida";
 RL Eur. J. Biochem. 247:545-557(1997).
 CC -1- FUNCTION: ANTIBACTERIAL AND ANTIVIRAL PEPTIDES THAT ADOPT AN ALPHA
 HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH
 CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY.
 CC -1- PTM: THE MAJOR PRODUCT IS CAERIN 1.1; IN ADDITION, DIFFERENT
 PEPTIDES ARE PRODUCED THAT ARE MISSING SOME AMINO ACID RESIDUES AT
 THE N-TERMINUS OR C-TERMINUS. ALL ISOFORMS ARE NOT REPRESENTED IN
 EACH SPECIES. CAERIN 1.1.1 AND CAERIN 1.1.4 ARE INACTIVE.
 CC -1- MASS SPECTROMETRY: MW-2382; METHOD-FAB; RANGE-1-25.
 CC -1- MASS SPECTROMETRY: MW-2412; METHOD-FAB; RANGE-3-25.
 CC -1- MASS SPECTROMETRY: MW-2299; METHOD-FAB; RANGE-4-25.
 CC -1- MASS SPECTROMETRY: MW-1421; METHOD-FAB; RANGE-13-25.
 CC -1- MASS SPECTROMETRY: MW-2333; METHOD-FAB; RANGE-1-23.
 CC -1- MASS SPECTROMETRY: MW-1826; METHOD-FAB; RANGE-1-16.
 CC -1- MASS SPECTROMETRY: MW-1489; METHOD-FAB; RANGE-1-15.
 CC -1- MASS SPECTROMETRY: MW-1180; METHOD-FAB; RANGE-1-12.
 CC -1- MASS SPECTROMETRY: MW-915; METHOD-FAB; RANGE-1-10.
 KW Antibiotic; Antiviral; Amphibian skin; Amidation.
 FT MOD_RES 1 25
 FT PEPTIDE 1 25
 FT PEPTIDE 3 25
 FT PEPTIDE 4 25
 FT PEPTIDE 13 25
 FT PEPTIDE 1 23
 FT PEPTIDE 1 16
 FT PEPTIDE 1 15
 FT PEPTIDE 1 12
 FT PEPTIDE 1 10
 FT MOD_RES 25 25
 SQ SEQUENCE 25 AA; 2585 MW; D8A5A460BB0EBE00 CRC64;

Query Match 20.8%; Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 LPRLIAFTSEH 15
 || : : ||
 DB 14 LPHVVPVIAEH 24

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.
 ID CR12_LITCE

AC P5G227;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CAERIN 1.3.
 OS Litoria caerulea.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID-30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea";
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY
 SIMILARITY).
 CC -1- MASS SPECTROMETRY: MW-2552; METHOD-FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 25 25
 FT SEQUENCE 25 AA; 2555 MW; D8A5A460BB1464C0 CRC64;
 SQ

Query Match 20.8%; Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 LPRLIAFTSEH 15
 || : : ||
 DB 14 LPHVVPVIAEH 24

RESULT 4
 CR13_LITCE STANDARD; PRT; 25 AA.
 ID CR13_LITCE
 AC P5G228;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CAERIN 1.3.
 OS Litoria caerulea.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID-30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea";
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY
 SIMILARITY).
 CC -1- MASS SPECTROMETRY: MW-2582; METHOD-FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 25 25
 FT SEQUENCE 25 AA; 2585 MW; D8A5A460BB0EA2F2 CRC64;
 SQ

Query Match 20.8%; Score 26; DB 1; Length 25;
Best Local Similarity 36.4%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 LPRLIATSEH 15
DB 14 LPHVPIYAEH 24

RESULT 5

CR14_LITIGI STANDARD; PRT; 25 AA.
AC P56229;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 1.4.
OS Litoria gilleni, and Litoria caerulea.
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=39405, 30344;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 1.4.
RC SPECIES=L.caerulea; TISSUE=Parotoid gland;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from Litoria caerulea."
RL J. Chem. Res. 138:910-936(1993).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 1.4.1.
RC SPECIES=L.gilleni; TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and CAERINs from Litoria gilleni."
RL J. Chem. Res. 139:937-961(1993).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS.
CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY SIMILARITY).
CC -1- MASS SPECTROMETRY: MW=2600; METHOD=FAB; RANGE=1-25.
CC -1- MASS SPECTROMETRY: MW=935; METHOD=FAB; RANGE=1-10.
KW Antibiotic; Amphibian skin; Amidation.
FT PEPTIDE 1 25 CAERIN 1.4.
FT PEPTIDE 1 10 CAERIN 1.4.1.
FT MOD_RES 25 25 AMIDATION
SQ SEQUENCE 25 AA; DBASBEBAVDB80E00 CRC64;

Query Match 20.8%; Score 26; DB 1; Length 25;
Best Local Similarity 36.4%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 LPRLIATSEH 15
DB 14 LPHVPIYAEH 24

RESULT 6
GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose."
RL Biochem. J. 123:25P-25P(1971).
CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPETIDE HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR; A03188; XGH0EU.
KW GLYCOPROTEIN.
FT CARBOHYD 1 1 S-LINKED (GAL. . .).
SQ SEQUENCE 8 AA; 855 MW; C2D87A1F5B1B1E CRC64;

Query Match 20.0%; Score 25; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ESHH 17
DB 2 ESHH 5

RESULT 7

FRE4_LITIN STANDARD; PRT; 24 AA.
AC P82023;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FRENATIN 4.
OS Litoria infrenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of the giant tree frog Litoria infrenata."
RL J. Pept. Sci. 2:117-124(1996).
CC -1- FUNCTION: WIDE SPECTRUM ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=2493; METHOD=FAB.
KW Antibiotic; Amphibian skin.
SQ SEQUENCE 24 AA; 2495 MW; 6986D063947805A1 CRC64;

Query Match 20.0%; Score 25; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
DB 6 LKKGAS 11

RESULT 8

CR15_LITCE STANDARD; PRT; 25 AA.
AC P56230;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE CAERIN 1.5.
OS Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=30344;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Parotoid gland;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea".
RL J. Chem. Res. 138:910-936(1993).
CC -1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
GLANDS.
CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY
SIMILARITY).
CC -1- MASS SPECTROMETRY: MW=2610; METHOD=FAB.
KW Antibiotic; Amphibian skin; Amidation.
FT MOD_RES 25 25
SQ SEQUENCE 25 AA; 2613 MW; 0FF5A464EA0E8E12 CRC64;

Query Match 19.2%; Score 24; DB 1; Length 25;
Best Local Similarity 27.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 5 LPRLIAFTSEH 15
DB 14 IPHYVPVIAEH 24

RESULT 9
VIP_GADMO VIP_GADMO STANDARD; PRT; 25 AA.
AC P09684;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE (VIP) (FRAGMENT).
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
OC Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RA Thwaites D.T., Young J., Thorndyke M.C., Dimaline R.;
RT "Isolation and characterisation of two teleost Vip's".
RL Regul. Pept. 21:436-436(1988).
CC -1- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
AND GALL BLADDER.
CC -1- MISCELLANEOUS: THERE IS ONLY A SINGLE DIFFERENCE BETWEEN THIS
SEQUENCE AND THAT OF CHICKEN (ALA-19 INSTEAD OF VAL-19).
CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; JQ0361.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2978 MW; 1573FF6F374DB7E4 CRC64;

Query Match 19.2%; Score 24; DB 1; Length 25;

Best Local Similarity 35.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 11 FTSESHFSLKKA 24
DB 6 FTDNYSRFRKQMAA 19

RESULT 10
PVK2_PERAM PVK2_PERAM STANDARD; PRT; 12 AA.
AC P81555;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PERIVISCEROKININ-2 (PEA-PVK-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE-Abdominal perisymphathetic organs;
RX MEDLINE=98326377; PubMed=9663444;
RA Fredel R., Rapus J., Eckert M., Holman G.M., Nachman R.J., Wang Y.,
Penzlin H.;
RT "Isolation of periviscerokinin-2 from the abdominal perisymphathetic
organs of the American cockroach, Periplaneta americana.";
RL Peptides 19:801-809(1998).
CC -1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITATORY ACTIONS ON THE
HYPERNEURAL MUSCLE.
CC -1- MASS SPECTROMETRY: MW=1189.3; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1190 MW; 2F4D8EE1EB05728 CRC64;

Query Match 18.4%; Score 23; DB 1; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.2e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMAALPRL 8
DB 5 GLISMPRV 12

RESULT 11
COM_CAVPO COM_CAVPO STANDARD; PRT; 22 AA.
AC P19069;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE COMPLEMENT C4 (FRAGMENT).
GN C4.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX MEDLINE=80227885; PubMed=7391069;
RA Goldberger G., Abraham G.N., Williams J., Colten H.R.;
RT "NH2-terminal sequence analysis of pro-C4, the precursor of the
fourth component of guinea pig complement.";
RL J. Biol. Chem. 255:7071-7074(1980).
CC -1- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
ANAPHYLATOXIN.
CC -1- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER

CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
 DR PIR: A17267; A17267.
 DR InterPro: IPR001599; Alpha_2_macroglubln.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; PARTIAL.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; PARTIAL.
 DR Complement pathway: Plasma; MHC III; Inflammatory response.
 FT VARIANT 18 18 L->V.
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA; 2452 MW; 2CD16B54D0B47A4 CRC64;

Query Match 18.4%; Score 23; DB 1; Length 22;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRLIAF 11
 DB 2 PRLILF 7
 RESULT 12
 CH60_THIFE STANDARD; PRT; 23 AA.
 AC P29134;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
 GN GROEL OR MOXA OR GROEL.
 OS Thiolobacillus ferrooxidans.
 OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
 ON NCBI_TaxID=920;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-ATCC 19859;
 RX MEDLINE=93093401; PubMed=1360930.
 RA Varela P., Jerez C.A.;
 RT "Identification and characterization of GroEL and DnaK homologues in Thiolobacillus ferrooxidans."
 RL FEBS Microbiol. Lett. 77:149-153(1992).
 RN [2]
 RP PHOSPHORYLATION.
 RX MEDLINE=96242312; PubMed=9026439;
 RA Seeger M., Osorio G., Jerez C.A.;
 RT "Phosphorylation of GroEL, DnaK and other proteins from Thiolobacillus ferrooxidans grown under different conditions."
 RL FEBS Microbiol. Lett. 138:129-134(1996).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS.
 CC -1- INDUCTION: BY HEAT SHOCK.
 CC -1- PTM: PHOSPHORYLATED ON THREONINE.
 CC -1- MISCELLANEOUS: THIS PROTEIN SHOWS ATPASE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR HSP; P06139; IAO.
 DR InterPro: IPR001844; Chaperonin cpn60.
 DR PROSITE: PS00296; CHAPERONIN_CP60; PARTIAL.
 KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2536 MW; 2BB6883872FB255D CRC64;

RESULT 13
 LMT4_LOCOMI STANDARD; PRT; 13 AA.
 ID LMT4_LOCOMI
 AC P14490;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LOCUSTAMYOTROPIN 4 (LOM-MT-4).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Cellifera;
 OC Acridoidea; Acrididae; Acrididae; Locusta.
 ON NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Looft A.;
 RT "Isolation, identification and synthesis of locustamytropin IIT and IIV, two additional neuropeptides of Locusta migratoria: members of the locustamytropin peptide family."
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE STIMULATOR THAN LOM-MT I, II AND III.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1553 MW; 2086194382AD6698 CRC64;

Query Match 17.6%; Score 22; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GMAALPRL 8
 DB 6 GMPSPRL 13
 RESULT 14
 CYCH_MOUSE STANDARD; PRT; 18 AA.
 ID CYCH_MOUSE
 AC 061458;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CYCLIN H (FRAGMENT).
 GN CCNH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-Testis;
 RA Hall F.L., Wu L.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MEMBER OF CAK WHICH ACTIVATES CYCLIN-ASSOCIATED CDC2/CDK2/CDK4 BY THREONINE PHOSPHORYLATION. ITS EXPRESSION AND ACTIVITY ARE CONSTANT THROUGHOUT THE CELL CYCLE. CAK IS TIGHTLY ASSOCIATED WITH A MULTIPROTEIN COMPLEX FTTH, WHICH PLAYS A DUAL ROLE IN TRANSCRIPTION AND DNA REPAIR (BY SIMILARITY).
 CC -1- SUBUNIT: MAMMALIAN CAK CONTAINS THREE COMPONENTS: CDK, CYCLIN H, AND AN ASSEMBLY FACTOR CALLED MAT1.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
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Query Match 18.0%; Score 22.5; DB 1; Length 23;
 Best Local Similarity 33.3%; Pred. No. 1.9e+03;
 Matches 5; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 9 IAFTESHSFSLKKG 23
 DB 5 VAF-AEHAREKMLRG 18

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DR EMBL; X82441; CAA57822.1; -
DR HSP; P51946; 1KXU.
DR InterPro; IPR000553; Cyclin.
DR PROSITE; PS00292; CYCLINS; PARTIAL.
KW Cyclin; Cell cycle; Cell division; Nuclear protein;
FT Transcription regulation.
FT NON_TER 1 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2105 MW; 92964DCF68EB98C7 CRC64;

Query Match 17.6%; Score 22; DB 1; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PRIIAFT 12
DB 10 PRIIMLT 16

RESULT 15
FAR7_ASCSU STANDARD; PRT; 8 AA.
ID FAR7_ASCSU STANDARD; PRT; 8 AA.
AC P43171;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE AF7.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.

RA MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum".
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 963 MW; 9CDA0059DA17687D CRC64;

Query Match 16.8%; Score 21; DB 1; Length 8;
Best Local Similarity 56.7%; Pred. No. 1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PRIIAF 11
DB 3 PRIIFR 8

RESULT 16
LPHI_ECOLI STANDARD; PRT; 16 AA.
ID LPHI_ECOLI STANDARD; PRT; 16 AA.
AC F03058;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HIS OPERON LEADER PEPTIDE (ATTENUATOR PEPTIDE).
GN HISL OR B2018.
OC Escherichia coli, and Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.
OX NCBI_TaxID=562, 602;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli, and S.typhimurium; STRAIN=K12, AND LT2;
RX MEDLINE=89094829; PubMed=3062174;
RA Carlomagno M.S., Chiarlotti L., Alfano P., Nappo A.G., Bruni C.B.;
RT "Structure and function of the Salmonella typhimurium and Escherichia
RL coli K-12 histidine operons".
RN J. Mol. Biol. 203:585-606(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=82039525; PubMed=6170941;
RA Verde P., Frunzio R., di Nocera P.P., Blasi F., Bruni C.B.;
RT "Identification, nucleotide sequence and expression of the regulatory
RT region of the histidine operon of Escherichia coli K-12".
RN Nucleic Acids. Res. 9:2075-2086(1981).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=79033821; PubMed=360215;
RA Dinocera P.P., Blasi F., Dillauro R., Frunzio R., Bruni C.B.;
RT "Nucleotide sequence of the attenuator region of the histidine operon
RT of Escherichia coli K-12".
RN Proc. Natl. Acad. Sci. U.S.A. 75:4276-4280(1978).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12".
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2;
RX MEDLINE=79033822; PubMed=360216;
RA Barnes W.M.;
RT "DNA sequence from the histidine operon control region: seven
RT histidine codons in a row".
RN Proc. Natl. Acad. Sci. U.S.A. 75:4281-4285(1978).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2;
RA Barnes W.M., Husson R.N., Whittier R.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN THE ATTENUATION MECHANISM
CC FOR THE CONTROL OF THE EXPRESSION OF THE HIS STRUCTURAL GENES.
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CC -----
DR EMBL; V00285; CAA23550.1; -
DR EMBL; V00284; CAA23548.1; -
DR EMBL; X13462; CAA31810.1; -
DR EMBL; V01371; CAA24656.1; -
DR EMBL; AE000293; AAC75079.1; -
DR EMBL; X13464; CAA31821.1; -
DR EMBL; J01804; AAA88613.1; -
DR PIR; A03594; LFECH.
DR EcoGene; EG11269; hisL.
DR StyGene; SG10166; hisL.
KW Histidine biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 16.8%; Score 21; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 9 IAFTESESH 17
DB 4 VOFKHHHH 12

RESULT 17
SETB_SALT
ID SETB_SALT STANDARD; PRT; 22 AA.

AC P33027;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SUGAR EFFLUX TRANSPORTER B (FRAGMENT).
GN SETB.

OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.

OX NCBI_TaxID=602;
RN [1]

RP MEDLINE-89313694; PubMed-2546043;
RX MEDLINE-89313694; PubMed-2546043;
RA Geeser R.H., Izso F., Postma P.W.;

RT "The PEP: fructose phosphotransferase system in Salmonella
typhimurium: FPR combines enzyme IIFru and pseudo-HPr activities.";

RL Mol. Gen. Genet. 216:517-525(1989).

CC -1- FUNCTION: INVOLVED IN THE EFFLUX OF SUGARS. THE PHYSIOLOGICAL ROLE
MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN
TRANSPORT LACTOSE AND GLUCOSE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
(PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE SET FAMILY OF TRANSPORTERS.

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CC EMBL: X14243; NOT ANNOTATED_CDS.
DR StyGene; SG10423; setB.

DR TRANSMEM 13 >22 POTENTIAL.
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2291 MW; 2849C30172CC5C2 CRC64;

Query Match 16.8%; Score 21; DB 1; Length 22;
Best Local Similarity 45.5%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 AALPRLAFTS 13
DB 7 AALPKSPDITS 17

RESULT 18
GAE6_RANRU
ID GAE6_RANRU STANDARD; PRT; 24 AA.

AC P80400;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GAE6URIN-6.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

OX NCBI_TaxID=8410;

RN [1]
RP SEQUENCE.

RC TISSUE-Skin;
RX MEDLINE-95091844; PubMed-7999137;

RA Park J.M., Jung J.-E., Lee B.J.;

RT "Antimicrobial peptides from the skin of a Korean frog, Rana
rugosa.";

RL Biochem. Biophys. Res. Commun. 205:948-954(1994).

CC -1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY. HAS A BROAD SPECTRUM OF
ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE BACTERIA,
FUNGI AND PROTOZOA.

CC -1- SUBUNIT: MONOMER.

CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- TISSUE SPECIFICITY: SKIN.

CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.

KW Amphibian skin; Antibiotic.
FT DISUPD 18 24
SQ SEQUENCE 24 AA; 2610 MW; 09918123FF90CCFD CRC64;

Query Match 16.8%; Score 21; DB 1; Length 24;
Best Local Similarity 54.5%; Pred. No. 3.5e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 1 GMAA-LPRLI 9
DB 7 GLAANFLPTII 17

RESULT 19
ALL1_CYPDPO
ID ALL1_CYPDPO STANDARD; PRT; 8 AA.

AC P82152;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CYDIASTASTIN 1.

OS Cydia pomonella (Coddling moth).

CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.

OX NCBI_TaxID=82600;

RN [1]

RP SEQUENCE.

RC TISSUE-Larva;

RX MEDLINE-98054539; PubMed-9392829;

RA Davey H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., East P.D., Thorpe A.;

RT "Lepidopteran peptides of the allatostatin superfamily.";

RL Peptides 18:1301-1309(1997).

CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 934 MW; C82879CA5B51F775 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 13 SEHSFSL 20
DB 1 SPHTNFGI 8

RESULT 20
GLEM_HUMAN
ID GLEM_HUMAN STANDARD; PRT; 10 AA.

AC P02728;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)
DE ERYTHROCYTE MEMBRANE GLYCOPROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72034940; PubMed=5286858;
RT Weiss J.B., Lote C.J., Bobinski H.;
RA "New low molecular weight glycoprotein containing triglycosylcysteine
in human erythrocyte membrane.";
RL Nature New Biol. 234:25-26(1971).
CC -!- PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.
CC -!- MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED.
CC PIR: A03187; XGHUE.
DR Glycoprotein; Erythrocyte.
KW CARBOHYD 1 1 S-LINKED (GLC. . .).
FT CARBOHYD 1 1 S-LINKED (GLC. . .).
SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B1E8 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 HSH 17
DB 4 HSH 6

RESULT 21
GONL_PETMA STANDARD; PRT; 10 AA.
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
(LULIBERIN I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey
brain.";
RL J. Biol. Chem. 261:4812-4819(1986).
CC -!- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
FOLLICLE-STIMULATING HORMONES.
CC -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR PIR: A01412; RHLNMG.
DR InterPro: IPR002012; Gnrh.
DR Pfam: PF00446; Gnrh; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 16.0%; Score 20; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 17 HSHLK 21
DB 2 HSHLE 6

RESULT 22
ASPL_LACSN STANDARD; PRT; 15 AA.
ID ASPL_LACSN
AC P82648;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ACID SHOCK PROTEIN 1 (FRAGMENT).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CBI;
RX PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 SLKKG 23
DB 1 SPKKG 5

RESULT 23
MCA2_RHOOP STANDARD; PRT; 15 AA.
ID MCA2_RHOOP
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE MALEYLACETATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=ICP;
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
Rhodococcus opacus ICP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -!- CATALYTIC ACTIVITY: 3-OXOADIPATE + NAD(P)(+) -> 2-MALEYLACETATE +
NAD(P)H.
CC -!- PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL-DEHYDROGENASE
FAMILY.
DR InterPro: IPR001670; Fe-ADH.
DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE: PS00060; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 16.0%; Score 20; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 LPR1AF 11
 11:11
 Db 8 LPR1XF 14

RESULT 24
 DFTS_RAT STANDARD; PRT; 20 AA.
 AC P07448;
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE DENTINAL FLUID TRANSPORT-STIMULATING PEPTIDE (DFT-STIMULATING PEPTIDE).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Parotid gland;
 RX MEDLINE=87131231; PubMed=3815601.
 RA Yamamoto T., Kobayashi M., Yamamoto M., Nomura M., Aonuma S.;
 RA "Isolation and amino acid sequence of dentinal fluid transport-stimulating peptide from rat parotid glands."
 RL Chem. Pharm. Bull. 34:3803-3811(1986).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=67131708; PubMed=5297832;
 RA Steinman R.R.;
 RA "The movement of acriflavine hydrochloride through molars of rats on RT a cariogenic and non-cariogenic diet."
 CC J. South Calif. Dent. Assoc. 35:151-157(1967).
 CC -1- FUNCTION: THIS PEPTIDE STIMULATES THE TRANSPORT OF DENTINAL FLUID, WHICH IS IMPORTANT FOR THE PREVENTION OF DENTAL CARIES.
 DR PIR: J00001; DIRT.
 KM Dental caries; Parotid gland; Hormone.
 SQ SEQUENCE 20 AA; 2165 MW; FA164F2B6AF80D5A CRC64;

Query Match 16.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 27.8%; Pred. No. 4.2e+03;
 Matches 5; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 QY 8 LIATSESHSLKGA 25
 11:11
 Db 2 VIAMELOHNEPGRDSTA 19

RESULT 25
 LPR1_BACST STANDARD; PRT; 20 AA.
 AC P05658;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TETRACYCLINE RESISTANCE LEADER PEPTIDE.
 GN TETL.
 OS Bacillus stearothermophilus, Bacillus cereus, and Staphylococcus hyicus.
 OG Plasmid pTH15, Plasmid pBC16, and Plasmid pSTEL.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Geobacillus.
 OX NCBI_TaxID=1422, 1396, 1284;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID-pTH15;
 RX MEDLINE=86031344; PubMed=2956983;
 RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
 RA "Nucleotide sequence of the tetracycline resistance gene of pTH15, a

RT thermophilic Bacillus plasmid: comparison with staphylococcal tcr RT controls.";
 RL Gene 37:131-138(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID-pBC16;
 RX MEDLINE=90221899; PubMed=21093312;
 RA Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pBC16 from Bacillus cereus."
 RL Nucleic Acids Res. 18:1635-1635(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=5-hyicus; PLASMID-pSTEL;
 RX MEDLINE=92321725; PubMed=1622166;
 RA Schwarz S., Cardoso M., Wegener H.C.;
 RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determinant encoded by plasmid pSTEL from Staphylococcus hyicus."
 RL Antimicrob. Agents Chemother. 36:580-588(1992).
 CC -----
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 CC -----
 DR EMBL: D00006; BAA00004.1; -
 DR EMBL: M11036; AAA2850.1; -
 DR EMBL: X51366; CAA35750.1; -
 DR EMBL: X60828; CAA43219.1; -
 DR PIR: S09233; LFBSRV.
 DR PIR: S23742; S23742.
 KM Leader peptide; Antibiotic resistance; Plasmid.
 SQ SEQUENCE 20 AA; 2253 MW; 18D0FA6CA231CA1 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 4.2e+03;
 Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 13 SEHSHFSLKGA 24
 11:11
 Db 4 NECNRVQLKGS 15

Search completed: January 6, 2002, 09:57:10
 Job time: 276 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: January 6, 2002, 09:51:49 ; Search time 22.2 Seconds
(without alignments)
164.721 Million cell updates/sec

Title: US-09-441-061-2
Sequence: 1 GMAALPRLIAFTSEHSFSLKGA 25

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SPTREMBL_17:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mmc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	25.6	25	2	O26056
2	30	24.0	20	6	P79837
3	27	21.6	25	10	O40354
4	26.5	21.2	24	7	O9TMS5
5	26	20.8	9	5	O9YV82
6	26	20.8	15	6	O9YV82
7	26	20.8	23	2	O9R314
8	26	20.8	24	4	O16333
9	25	20.0	15	11	O92003
10	25	20.0	23	5	O9NBD9
11	25	20.0	23	12	O87081
12	25	20.0	24	4	O16061
13	25	20.0	24	13	P82833
14	25	20.0	24	13	P82833
15	25	20.0	24	13	P82833
16	25	20.0	24	13	P82833
17	25	20.0	25	4	O9BTR5
18	25	20.0	25	11	O60839
19	25	20.0	25	11	O63999
20	25	20.0	25	11	O64000

20	25	20.0	25	12	O9YV4	O9YV14 lucerne tra
21	24	19.2	15	4	O16158	O16158 homo sapien
22	24	19.2	16	4	O9UC55	O9UC55 homo sapien
23	24	19.2	17	4	O9BTR2	O9BTR2 homo sapien
24	24	19.2	18	5	O9TMS7	O9TMS7 lamellibrac
25	24	19.2	18	5	O9PMS7	O9PMS7 oncorhynch
26	24	19.2	22	13	O9K8Q3	O9K8Q3 bacillus ha
27	24	19.2	22	13	O9W6D7	O9W6D7 gallus gall
28	24	19.2	24	10	O9ZS60	O9ZS60 lycopersico
29	24	19.2	25	5	O9M59	O9M59 sagitta sp.
30	23	18.8	17	11	O9CVP3	O9CVP3 mus musculu
31	23	18.4	11	4	O9UQJ1	O9UQJ1 homo sapien
32	23	18.4	11	5	P82699	P82699 leucophaea
33	23	18.4	12	6	O9WZS4	O9WZS4 canis fami
34	23	18.4	12	10	O9ZNT6	O9ZNT6 oryza brach
35	23	18.4	15	6	P82665	P82665 bos taurus
36	23	18.4	16	2	O48439	O48439 klebsiella
37	23	18.4	16	4	O9UWJ9	O9UWJ9 homo sapien
38	23	18.4	16	4	O9NN22	O9NN22 homo sapien
39	23	18.4	16	12	O04246	O04246 human para
40	23	18.4	17	2	O34216	O34216 pseudomonas
41	23	18.4	18	2	O92G42	O92G42 chlamydia t
42	23	18.4	18	5	O26833	O26833 trypanosoma
43	23	18.4	21	4	O14595	O14595 homo sapien
44	23	18.4	21	11	O9QV63	O9QV63 arabidopsis
45	23	18.4	22	10	O9SY23	O9SY23 rattus sp.
46	23	18.4	22	11	O9R1C1	O9R1C1 mus musculu
47	23	18.4	23	2	O9L8A4	O9L8A4 rhododactyl
48	23	18.4	23	11	O9J1N0	O9J1N0 mus musculu
49	23	18.4	24	13	P82825	P82825 rana tuteiv
50	23	18.4	25	2	O9R5G2	O9R5G2 lactobacill

ALIGNMENTS

RESULT 1
ID O26056 PRELIMINARY; PRT; 25 AA.
AC O26056;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DI 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOTHEICAL 3.1 KDA PROTEIN.
GN HP1528.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McMeney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Meldrum J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AEO00651; AAD08577.1; -
DR TIGR; HP1528; -
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 25 AA; 3075 MW; E080E33A1CE396E CRC64;

Query Match 25.6%; Score 32; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;

Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 8 LIAFTSEHSFLSKG 23
 ||| :|||
 Db 2 LIRYFRFLDLSLKG 17

RESULT 2

P79837 ID P79837 PRELIMINARY; PRT; 20 AA.
 AC P79837
 DT 01-MAY-1997 (TREMREL. 03, Created)
 DT 01-MAY-1997 (TREMREL. 03, Last sequence update)
 DT 01-MAY-1997 (TREMREL. 03, Last annotation update)
 DE IDURONATE 2-SULFATASE (FRAGMENT).
 OS Prionailurus bengalensis (leopard cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
 OX NCBI_TaxID=37029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
 RA O'Brien S.J.,
 RL Nat. Genet. 15:0-0(0).
 DR EMBL: U81266; AB39359.1; -.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2081 MW; 7D009D35F57AE228 CRC64;

Query Match 24.0%; Score 30; DB 6; Length 20;
 Best Local Similarity 62.5%; Pred. No. 4.5e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 LIAFTSEH 15
 :||| :|||
 Db 13 IIAFASDH 20

RESULT 3

Q40354 ID Q40354 PRELIMINARY; PRT; 25 AA.
 AC Q40354
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
 DE MOS GENE (REQUIRED FOR SYNTHESIS OF L-3-O-METHYL-SCYLLO-INOSAMINE
 DE (3-O-MSI)), 5' END AND PROMOTER REGION (FRAGMENT).
 GN MOS.
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89057889; PubMed=2848255;
 RA Murphy P.J., Heycke N., Trenz S.P., Ratet P., De Bruijn F.J.,
 RA Schell J.;
 RT "Synthesis of an opine-like compound, a rhizopine, in alfalfa nodules
 RT is symbiotically regulated."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:9133-9137(1988).
 DR EMBL: M23347; AAA32661.1; -.
 DR InterPro: IPR000392; NitrogenaseII.
 DR Pfam: PF00142; fer4_NiHf. 1.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2685 MW; 1F22739287210F82 CRC64;

Query Match 21.6%; Score 27; DB 10; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ALPRLIAF 11
 | | | | |
 Db 2 AAPRQIAF 9

RESULT 4

Q9TNS5 ID Q9TNS5 PRELIMINARY; PRT; 24 AA.
 AC Q9TNS5
 DT 01-MAY-2000 (TREMREL. 13, Created)
 DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
 DT 01-JUN-2000 (TREMREL. 14, Last annotation update)
 DE HUMAN LEUCOCYTE ANTIGEN BETA CHAIN DR MOLECULE HLA-DRB1 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93107319; PubMed=1469092;
 RA Weyand C.M., Hicok K.C., Hunder G.G., Goronzy J.J.;
 RT "The HLA-DRB1 locus as a genetic component in giant cell arteritis.
 RT Mapping of a disease-linked sequence motif to the antigen binding site
 RT of the HLA-DR molecule."
 RL J. Clin. Invest. 90:2355-2361(1992).
 KW MHC.
 SQ SEQUENCE 24 AA; 3019 MW; 4A23BF7821BACCE0 CRC64;

Query Match 21.2%; Score 26.5; DB 7; Length 24;
 Best Local Similarity 41.2%; Pred. No. 2e+03;
 Matches 7; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 12 TSEHSFHS-----LKKG 23
 ||| :|||
 Db 5 TSEYDFPHNDAYLQKG 21

RESULT 5

Q9VV82 ID Q9VV82 PRELIMINARY; PRT; 9 AA.
 AC Q9VV82
 DT 01-MAY-2000 (TREMREL. 13, Created)
 DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
 DE CG18219 PROTEIN (FRAGMENT).
 GN CG18219.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champ C.R., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.A., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Rosler C., Evangelista A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Meriklov G., Milstina N.V., Modarity C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimas I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Switskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL, AF003526; AAF9437.1;
 DR FlyBase; FBgn0036647; CG18219.
 FT NON-TER
 SO SEQUENCE 9 AA; 975 MW; F31AB4472045B9C1 CRC64;

Query Match 20.8%; Score 26; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 4.7e+05;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 16 SHESLKKA 24
 DB 1 SHESLNSA 9

RESULT 6
 O9TRPO PRELIMINARY; PRT; 15 AA.
 AC 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE LOW MR ZONA PELLUCIDA BINDING PROTEIN (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP MEDLINE=92378826; PubMed=1510840;
 RA Parry R.V., Barker P.J., Jones R.,
 RT "Characterization of low Mr zona pellucida binding proteins from boar
 RL Mol. Reprod. Dev. 33:108-115(1992).
 SO SEQUENCE 15 AA; 1525 MW; CC80DE1028CF2058 CRC64;

Query Match 20.8%; Score 26; DB 6; Length 15;
 Best Local Similarity 44.4%; Pred. No. 1.5e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 3 AALPRLIAF 11
 DB 7 AALPSVVF 15

RESULT 7
 O9R314 PRELIMINARY; PRT; 23 AA.
 AC 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update).
 DE DNA ADENINE METHYLASE HOMOLOG (FRAGMENT).
 GN M.HPT.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=219, AND 213;
 RA Raudoniklene A., Berg D.E.,
 RT "Icxa2 segment from H. pylori (Alaska strain 219)."
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF008929; AAC64502.1;
 DR EMBL; AF008928; AAC64500.1;
 KW Methyltransferase.
 FT NON-TER
 SO SEQUENCE 23 AA; 2635 MW; 6D6CC63737422B3 CRC64;

Query Match 20.8%; Score 26; DB 2; Length 23;
 Best Local Similarity 45.5%; Pred. No. 2.4e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 7 RLIAFTSESH 17
 DB 9 KLIPFIKENIH 19

RESULT 8
 ID 016333 PRELIMINARY; PRT; 24 AA.
 AC 016333;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR (FRAGMENT).
 GN FLT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95222657; PubMed=7707437;
 RA Bocock C.A., Charnock-Jones D.S., Sharkey A.M., McLaren J.,
 RA Barker P.J., Wright K.A., Twytlman P.R., Smith S.K.,
 RT "Expression of vascular endothelial growth factor and its receptors
 RL flt and KDR in ovarian carcinoma."
 RL J. Natl. Cancer Inst. 87:506-516(1995).
 DR EMBL; S77814; AAB34002.1;
 FT NON-TER
 SO SEQUENCE 24 AA; 2700 MW; 993CFEB9FE226A62 CRC64;

Query Match 20.8%; Score 26; DB 4; Length 24;
 Best Local Similarity 44.4%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 10 APTSESHF 18
 DB 14 SFSNTEHF 22

RESULT 9
 O92003 PRELIMINARY; PRT; 15 AA.
 AC 092003;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE SNO ONCOPROTEIN (FRAGMENT).
 GN SNO.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vedoy C.G., Sogayar M.C.;
 RT "Cloning of glucocorticoid-regulated sequences using equalizing cDNA
 RT subtraction based on selective suppression of polymerase chain
 RT reaction in rat C6/Srl glioma phenotypic reversion.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF112446; AAD17200.1;
 DR EMBL: AF112446; AAD17200.1;
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1667 MW; D2F5236DE2647B80 CRC64;

Query Match 20.0%; Score 25; DB 11; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.2e+03;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 SHFSLKKA 24
 :||| :|
 Db 6 SNFSLVQGS 14

RESULT 10
 Q9NBD9 ID Q9NBD9 PRELIMINARY; PRT; 23 AA.
 AC Q9NBD9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HEMOGLOBIN IIB (FRAGMENT).
 GN GB28.
 OS Chironomus nepeanensis.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=113501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20336639; PubMed=10876092;
 RA Gruhl M.C., Scherbak S.V., Amanova K.G., Blinov A., Diez J.-L.,
 RA Bergtrom G.;
 RT "Insect globin gene polymorphisms: Intronic minisatellites and a
 RT retroposon interrupting exon 1 of homologous globin genes in
 RT Chironomus (Diptera).";
 RL Gene.251:153-163(2000).
 DR EMBL: AF250305; AAF87114.1;
 DR EMBL: AF250305; AAF87114.1;
 FT NON_TER 1 1
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2333 MW; 3B08F7A8FAB5EF33 CRC64;

Query Match 20.0%; Score 25; DB 5; Length 23;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 RLIAFTSE 14
 :| :| :|
 Db 6 RIVGFVSE 13

RESULT 11
 Q87081 ID Q87081 PRELIMINARY; PRT; 23 AA.
 AC Q87081;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE GLYCOPROTEIN C PRECURSOR (FRAGMENT).
 GN GC.
 OS Pseudorabies virus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10345;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BECKER;
 RX MEDLINE=96070924; PubMed=7499261;
 RA Ryan P., Edwards C.O.;
 RT "Systematic introduction of proline in a eukaryotic signal sequence
 RT suggests asymmetry within the hydrophobic core.";
 RL J. Biol. Chem. 270:27876-27879(1995).
 DR EMBL: U29124; AAC54534.1;
 DR EMBL: U29124; AAC54534.1;
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2229 MW; B7112B05ED406F3F CRC64;

Query Match 20.0%; Score 25; DB 12; Length 23;
 Best Local Similarity 66.7%; Pred. No. 3.4e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAALPLRIA 10
 :||| :|
 Db 8 MLALPALYA 16

RESULT 12
 Q16061 ID Q16061 PRELIMINARY; PRT; 24 AA.
 AC Q16061;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE TNNT1 PROTEIN (FRAGMENT).
 GN TNNT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94006957; PubMed=8403232;
 RA Novelli G., Gennarelli M., Sangiulio F., D'Agruma L., Lo Cicero S.,
 RA Melchionda S., Dallapiccola B.;
 RT "Isolation and cloning by a polymerase chain reaction of a genomic DNA
 RT fragment of the human slow skeletal troponin (TNNT1) gene.";
 RL Cell Biochemistry and Function 11:187-191(1993).
 DR EMBL: S66057; AAD13978.1;
 DR EMBL: S66170; AAD13978.1; JOINED.
 FT NON_TER 24 24
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2742 MW; 4A41B1A59FD34E5E CRC64;

Query Match 20.0%; Score 25; DB 4; Length 24;
 Best Local Similarity 55.6%; Pred. No. 3.6e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 SHFSLKKA 24
 :| :| :| :|
 Db 6 SHAAKRGKA 14

RESULT 13
 P82833 ID P82833 PRELIMINARY; PRT; 24 AA.
 AC P82833;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BREVININ-1BA.
 GN BREVININ-1BA.
 OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_Taxid=30360;
 RM [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE=20117700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 isolated from the skins of the North American frogs Rana luteiventris,
 Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 S. AUREUS.
 CC -1- MASS SPECTROMETRY: MM=2643; METHOD-ELECTROSPRAY.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 KW Antibiotic.
 FT DISULFID
 SO SEQUENCE 24 AA; 2645 MW; CB524A454471DF4 CRC64;
 BY SIMILARITY.

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03;
 Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

OY 1 GMAA--LPRLIATSE 14
 |||||
 DB 7 GMAAKPLKIFCAISK 22

RESULT 14

P82834 PRELIMINARY; PRT; 24 AA.
 AC P82834;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE BREVININ-1B.
 OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 RN NCBI_Taxid=30360;
 RM [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE=20117700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 isolated from the skins of the North American frogs Rana luteiventris,
 Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 S. AUREUS AND GRAM-NEGATIVE BACTERIUM E. COLI. ACTIVE AGAINST
 C. ALBICANS.
 CC -1- MASS SPECTROMETRY: MM=2567.3; METHOD-ELECTROSPRAY.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 KW Antibiotic; Fungicide.
 FT DISULFID 18 24
 SO SEQUENCE 24 AA; 2569 MW; CB524A454471DF4 CRC64;
 BY SIMILARITY.

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03;
 Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

OY 1 GMAA--LPRLIATSE 14
 |||||
 DB 7 GMAAKPLKIFCAISK 22

RESULT 15

P82838 PRELIMINARY; PRT; 24 AA.
 AC P82838;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE BREVININ-1B.
 OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 RN NCBI_Taxid=30360;
 RM [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE=20117700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 isolated from the skins of the North American frogs Rana luteiventris,
 Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 S. AUREUS AND GRAM-NEGATIVE BACTERIUM E. COLI.
 CC -1- MASS SPECTROMETRY: MM=2629; METHOD-ELECTROSPRAY.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 KW Antibiotic.
 FT DISULFID 18 24
 SO SEQUENCE 24 AA; 2631 MW; CB524A4544434CF4 CRC64;
 BY SIMILARITY.

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03;
 Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

OY 1 GMAA--LPRLIATSE 14
 |||||
 DB 7 GMAAKPLKIFCAISK 22

RESULT 16

O9BTR5 PRELIMINARY; PRT; 25 AA.
 AC O9BTR5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE UNKNOWN (PROTEIN FOR IMAGE:3451138) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_Taxid=9606;
 RM [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CHORIOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003414; AA03414.1;
 FT NON_TER 1 1
 SO SEQUENCE 25 AA; 2825 MW; 8B6494418A85ABD5 CRC64;

Query Match 20.0%; Score 25; DB 4; Length 25;
 Best Local Similarity 80.0%; Pred. No. 3.8e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 13 SEHSH 17
 |||||
 DB 13 SEKH 17

RESULT 17

Q60839	Q60839	PRELIMINARY;	PRT;	25 AA.
ID	Q60839			
AC	Q60839			
DT	01-NOV-1996	(TReMBLrel. 01, Created)		
DT	01-NOV-1996	(TReMBLrel. 01, last sequence update)		
DT	01-AUG-1998	(TReMBLrel. 07, last annotation update)		
DE	ALPHA-1-ACID GLYCOPROTEIN-2 (FRAGMENT).			
DE	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C; TISSUE=LIVER;			
RA	Merchant M.E., Keherly M.J., Mifflin R.C., Papaconstantinou J.;			
RL	Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U24278; AAA91124.1;			
NR	NON_TER			
FT	25			
SQ	SEQUENCE 25 AA: 2843 MW.			

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Query Match      20.0%;      Score 25;  DB 11;      Length 25;
Best Local Similarity 38.5%;      Pred. No. 3.8e+03;
Matches 5;  Conservative 4;  Mismatches 4;  Indels 0;  Gaps 0;

QY      8  LIAFTSEHSHFSL 20
      | | | | |
DB      2  LEAQNPEHANFTI 14

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RESULT      18
Q63999     Q63999          PRELIMINARY;                PRT;        25 AA.
AC         Q63999;
DT         01-NOV-1996 (TRENBLrel. 01, Created)
DT         01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT         01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE         VASOPRESSIN (FRAGMENT).
OS         Rattus norvegicus (Rat).
OC         Zukaryotka; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX         NCBI_TaxID=10116;
RN         [1]
RP         SEQUENCE FROM N.A.
RX         MEDLINE=94286576; PubMed=8016115;
RA         Evans D.A., der Kleij A.A., Sonnemans M.A., Burbach J.P.,
RV         Van Leeuwen F.W.;
RT         "Frameshift mutations at two hotspots in vasopressin transcripts in
RL         post-mitotic neurons.";
RT         Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063(1994).
RD         EMBL; S71426; AAB31127.1; -.
DR         NON_TER
SQ         SEQUENCE      1
FT         SEQUENCE    25 AA; 2478 MW; 4D78687ACFC63FE9_CDC64.
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Query Match      20.8%      Score 25; DB 11; Length 25;
Best Local Similarity 75.0%; Pred. No. 3.8e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AALPRLIA 10
        |||||
Db       4 AALPRASA 11

RESULT 19
Q64000
ID Q64000 PRELIMINARY; PRT; 25 AA.
AC Q64000;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE VASOPRESSIN (FRAGMENT).
OS Rattus norvegicus (Rat).

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OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC	NCBI_TaxID=10116;
RP	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94286576; PubMed=8016115;
RA	Evans D.A., der Kleij A.A., Sonnemans M.A., Burbach J.P.,
RA	Van Leeuwen F.W.;
RT	"Frameshift mutations at two hotspots in vasopressin transcripts in
RT	post-mitotic neurons.";
RL	Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063(1994).
DR	EMBL; S71427; AAB31128.1; -;
FT	NON TER 1
SQ	SEQUENCE 25 AA; 2455 MW; B1F1E5E4D310F237 CRC64;

Query Match	20.0%;	Score 25;	DB 11;	Length 25;
Best Local Similarity	75.0%;	Pred. No. 3.8e+03;		

Query Match	20.0%	score 25;	DB 11;	Length 25;
Best Local Similarity	75.0%;	Pred. No. 3.8e+03;		
Matches	6;	Conservative	0;	Mismatches 2;
		Indels	0;	Gaps 0;
QY	3	AALPRLIA	10	
DB	4	AALPRASA	11	

RESULT	20
Q9YFJ4	
ID	PRELIMINARY;
AC	Q9YPJ4
CD	Q9YPJ4;
DT	01-MAY-1999 (TReMBIrel. 10, Created)
DT	01-MAY-1999 (TReMBIrel. 10, Last sequence update)
DT	01-MAY-1999 (TReMBIrel. 10, Last annotation update)
DE	LTSV-C) RNA2, COMPLETE.
OS	Lucerne transient streak virus.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Sobemovirus.
OX	NCBI_TaxID=12470;
RX	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=86089532; PubMed=3335832;
RA	Abouhaïdar M.G., Pallwal Y.C.;
RT	"Nucleotide sequence of the capsid protein gene and 3' non-coding'
RT	region of papaya mosaic virus RNA.";
RL	J. Gen. Virol. 69:2369-2373(1988).
DR	EMBL: D00341; BRAU0227.f.; -
RD	SEQUENCE 25 AA; 2868 MW; DCCE463D3B83C383 CRC64:
SQ	

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Query Match          20.0%;      Score 25;  DB 12;      Length 25;
Best Local Similarity 46.3%;      Pred. No. 3.8e+03;
Matches 6;  Conservative 2;  Mismatches 0;  Gaps 0;
QY      9  IAFTEHSHFSLK 21
        ::|||
DB      11  VSHTERDTRSLK 23
        ::|||

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RESULT	21
Q16158	
ID	PRELIMINARY;
AC	Q16158; PRT; 15 AA.
DT	01-NOV-1996 (TRENBLrel. 01, Created)
DT	01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT	01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE	C-MYC PROTEIN (FRAGMENT).
GN	C-MYC.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94238920; PubMed=8182948;
RA	Brennscheidt U., Eck D., Kunzmann R., Martens U., Kiehnopf M.,

RA Metelmann R., Herrmann F.;
 RT "Burkitt-like mutations in the c-myc gene locus in Prolymphocytic
 RL Leukemia." 8:897-902(1994).
 DR EMBL, S70386; AAB30748.1; -
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1772 MW; 883PB769FC6D5A98 CRC64;

Query Match
 Best Local Similarity 19.2%; Score 24; DB 4; Length 15;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 5 LPRLAFTSEH 15
 DB 1 MPLNVSFTSRN 11

RESULT 22
 ID Q9UC55 PRELIMINARY; PRT; 16 AA.
 AC Q9UC55;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 14, Last annotation update)
 DE PROTEIN C OSAKA 10 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-96124381; PubMed-8560401;
 RA Miyata T., Zheng Y.Z., Sakata T., Kato H.;
 RT "Protein C Osaka 10 with aberrant propeptide processing: loss of
 RT anticoagulant activity due to an amino acid substitution in the
 RL Thromb. Haemost. 74:1003-1008(1995).
 SQ SEQUENCE 16 AA; 1875 MW; EBD5F581F3D325244 CRC64;

Query Match
 Best Local Similarity 19.2%; Score 24; DB 4; Length 16;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 10 AFTSEHSRSLK 22
 DB 4 SFLELRHSLER 16

RESULT 23
 ID Q9BYF2 PRELIMINARY; PRT; 17 AA.
 AC Q9BYF2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE RIBOSOMAL PROTEIN L39 (FRAGMENT).
 GN RPL39.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Uechi T., Tanaka T., Kenmochi N.;
 RT "A complete map of the human ribosomal protein genes: assignment of 80
 RL genes to the cytosolic map and implications for human disorders.";
 DR EMBL, AB046411; BAB21257.1; -
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2107 MW; 8398CFA38BD5FA9A CRC64;

Query Match
 Best Local Similarity 19.2%; Score 24; DB 4; Length 17;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 13 SEHSRSLK 22
 DB 2 SSKTRPRIRK 11

RESULT 24
 ID Q9TWS7 PRELIMINARY; PRT; 18 AA.
 AC Q9TWS7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE 44 KDA HEMOGLOBIN B1 CHAIN (FRAGMENT).
 OS Lamellibranchia sp. (Deep-sea giant tube worm).
 OC Eukaryota; Metazoa; Vestimentifera; Basidibranchia; Lamellibranchiida;
 OC Lamellibranchiidae; Lamellibranchia.
 OX NCBI_TaxID=6424;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-93320735; PubMed-7763791;
 RA Suzuki T., Takagi T., Ohta S.;
 RL Zool. Sci. 10:141-146(1993).
 SQ SEQUENCE 18 AA; 2192 MW; 039D56A0B814670F CRC64;

Query Match
 Best Local Similarity 19.2%; Score 24; DB 5; Length 18;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 13 SEHSRSLK 18
 DB 3 SDCHX 8

RESULT 25
 ID Q9PS15 PRELIMINARY; PRT; 20 AA.
 AC Q9PS15;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CREATINE KINASE (EC 2.7.3.2) (FRAGMENT).
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93080727; PubMed-1449598;
 RA White K.C., Babbitt P.C., Buechter D.D., Kenyon G.L.;
 RT "The principal islet of the Coho salmon (Oncorhynchus kisutch) contains
 RL the BB isoenzyme of creatine kinase.";
 DR HSSP; P00563; 2CKK.
 SQ SEQUENCE 20 AA; 2425 MW; BFB071D6D2A86E11 CRC64;

Query Match
 Best Local Similarity 19.2%; Score 24; DB 13; Length 20;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 11 FTSEHSRSLK 20
 DB 2 FGNTNNRKL 11

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